

STIC-Biotech/ChemLib

154743

11/12/05

From: Bunner, Bridget
Sent: Friday, May 27, 2005 10:09 AM
To: STIC-Biotech/ChemLib
Subject: sequence search

Hi! I'd like to request a sequence search for case 10/777,524:

1. the amino acid sequence of SEQ ID NO: 2

Thanks!

Bridget Bunner

Art Unit 1647
Rem 4C65
(571) 272-0881
mailbox 4C70

RECEIVED
MAY 27 2005
STIC

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2- _____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA#: _____ AA#: _____
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIS: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 1, 2005, 22:01:20 ; Search time 40 Seconds

(without alignments)
728.842 Million cell updates/sec

Title: US-10-777-524-2

Perfect score: 1591

Sequence: 1 MGRPLRLPLRLPLRLPLRLQ.....PSHRLKSPQNETLXSVLKA 303

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1.*

2: p1r2.*

3: p1r3.*

4: p1r4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	144.5	9.1	823	2	S48394
2	123.5	7.8	1114	2	T49517
3	118.5	7.4	509	2	JC5288
4	116	7.3	392	2	B44194
5	115.5	7.3	417	2	A44194
6	115.5	7.3	513	2	JC5289
7	114	7.2	392	1	RWHUPD
8	114	7.2	417	1	RWHUPA
9	112.5	7.1	403	2	S25750
10	110	6.9	235	2	S25758
11	110	6.9	847	2	JH0371
12	108.5	6.9	233	2	S25747
13	108.5	6.8	230	2	S49449
14	108.5	6.8	235	2	S14675
15	108.5	6.8	862	2	I49583
16	108.5	6.8	868	2	A46512
17	108	6.8	236	2	S25746
18	108	6.8	1694	2	S50065
19	106	6.7	647	2	A93648
20	106	6.7	710	2	A99486
21	105.5	6.6	235	2	S25750
22	104.5	6.6	214	2	PC4156
23	104	6.5	231	2	S25751
24	104	6.5	798	2	T34248
25	103	6.5	446	2	T45525
26	103	6.5	469	2	S37483
27	102.5	6.4	407	2	T08732
28	102	6.4	572	2	B46529
29	101	6.3	118	2	E27889

30	101	6.3	790	2	T34293	hypothetical prote
31	100.5	6.3	151	2	T46626	rearranged T-cell
32	100.5	6.3	152	2	B26471	Ig heavy chain pre
33	100	6.3	365	2	A47636	MHC class I h1etoc
34	100	6.3	365	2	I83063	A11.2 - human
35	100	6.3	365	2	I37478	MHC class I histoc
36	99.5	6.3	413	2	T04520	hypothetical prote
37	99	6.2	210	2	S25657	T-cell surface gly
38	99	6.2	231	2	S25728	Ig lambda chain -
39	99	6.2	232	2	S25756	Ig lambda chain -
40	98	6.2	217	2	JE0246	Ig lambda chain NI
41	98	6.2	235	2	S25759	Ig lambda chain -
42	97	6.1	142	2	A28344	VpreB protein prec
43	97	6.1	229	2	A20969	Ig kappa chain pre
44	97	6.1	365	2	T16961	MHC class I protei
45	97	6.1	1272	2	S26180	neurofascin - ch1c

ALIGNMENTS

RESULT 1

S48394 probable membrane protein Y11410W - Yeast (Saccharomyces cerevisiae)

C:Species: Saccharomyces cerevisiae

C>Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 09-Jul-2004

C:Accession: S48394; S50276

R:Churher, C.

submitted to the EMBL Data Library, September 1994

A:Reference number: S48310

A:Accession: S48394

A:Molecule type: DNA

A:Residues: 1-823 <CHU>

A:Cross-references: UNIPROT:P38928; GB:Z47047; EMBL:Z38059; NID:9603997; PID:9763206; MI

R:Torpey, L.E.; Gibbs, P.E.M.; Nelson, J.; Lawrence, C.W.

Yeast 10, 1503-1509, 1994

A>Title: Cloning and sequence of REV7, a gene whose function is required for DNA damage-

A:Reference number: S50275; MUID:95176709; PMID:7871890

A:Accession: S50276

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 80-823 <TOR>

A:Cross-references: EMBL:U07228; NID:9460247; PID:NAA67919.1; PID:9460249

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1994

C:Genetics:

A:Gene: SGD:SRO4

A:Cross-references: SGD:S0001402; MIPS:Y11410W

A:Map position: 9L

C:Superfamily: Saccharomyces cerevisiae probable membrane protein Y11410W

C:Keywords: transmembrane protein

F:6-22/Domain: transmembrane #status predicted <TM1>

F:511-527/Domain: transmembrane #status predicted <TM2>

Query Match 9.1%; Score 144.5; DB 2; Length 823;

Best local similarity 24.7%; Pred. No. 0.0026; Matches 72; Conservative 45; Mismatches 96; Indels 79; Gaps 16;

QY	25	TGSGPSYLYGV-TOPKILASM--GGSVEIPFSFYPMELATADV-----RISMR	73
DB	308	SGSVPEDELKGNNSPANSVSIYDTYGDV-----IYFVEVSTPDLFAISLPLNINATR	362
QY	74	GHPFGQSFSTRPFSIHQDYNR---LFLN-----WTEGQK-----GFLRIS	113
DB	363	GEWFSYFL---PSQFTDYNTVSLFTNSSQDHPMKQSSNLTLAGEVPPKPFULS	418
QY	114	-----NLQKQSVYFCFVELDTRSSGROQCSIEGTGLSTTQAVTTTTPORPSMTTWR	168
DB	419	LGLRANQSQSDELYFNIGMDSKITHSNHANTSTRSS---HHSISTSYTSSTYAK	475
QY	169	LSSTT---TTTGLRVTQGRKRSDSMHSLETVAGVAVAVTV-LGIMTGLIC-LRRMR	223
DB	476	ISSTSAATSSAPALPAANKTSSHN---KKAVALACGVALPLGLIIVALICPLIPWRR	532

RESULT 5

A44194

poliovirus receptor (clone AGM-alpha-1) - green monkey

C|Species: Cercopithecus aethiops (green monkey, grivet)

C|Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C|Accession: A44194

C|Citation: A44194

R|Koike, S.; Ise, I.; Sato, Y.; Yonekawa, H.; Gotoh, O.; Nomoto, A.

J|Vol. 66, 7059-7066, 1992

A|Title: A second gene for the African green monkey poliovirus receptor that has no putative reference number: A44194; MUID:93059651; PMID:1331508

A|Accession: A44194

A|Status: preliminary

A|Molecule type: DNA

A|Residues: 1-417 <KOI>

A|Cross-references: UNIPROT:P32506; GB:S48777

C|Superfamily: poliovirus receptor; Immunoglobulin homology

C|Keywords: transmembrane protein

F|259-314/Domain: Immunoglobulin homology <IMM>

Query Match 7.3%; Score 116; DB 2; Length 417;

Best Local Similarity 21.2%; Pred. No. 0.18; Mismatches 110; Indels 134; Gaps 16;

Matches 77; Conservative 42; Mismatches 110; Indels 134; Gaps 16;

QY 4 PLLPLPLPLPPAFLQPSGSGPSYLYGVTPKHLASMGSGSVLPFSFYPMELAT 63

DB 11 PLLTLLELSWPP-----PGTGDI--VQAPTVPGFLGDSVTLPCYLQVGMDET 59

QY 64 APDVRISRRGHFGQS-----FYSTRPSIHKOYVNRFLPNTMGCKSGF----- 109

DB 60 HVS-QLTWSR--HESGSMVAFHOTGP-----NYSEPKLEFVAARLTTEL 103

QY 110 ----LRISNLKQDQSVFC-----RYELDTRSSGQQWQSIEGTLKSI 149

DB 104 RDAELRMGLAVEDEGNATCLFVTFPGSSRVDTMLKRLAPQNTAFVQKQLGKVPV 163

QY 150 TQAVTTTQRPSSMTTWK-----LSSTTTTGLATVGKRRSDS----- 189

DB 164 ARCVSTGSRPAHI--TWHSDLGGMPTSQAPGFLSGVITVTSIMLIPSSQVDGKSVTC 221

QY 190 --WHISLETAVGVAVTVVLGIMILGLICLRMRKRGQOKTKATTPARBPQWTEPEYE 247

DB 222 KVEHSEFEKPOLLTNLTIVY-----YPEVSIISGYD 252

QY 248 N----INNEGONT--DPKLNPKDDGIVYASLALSSSTSPRPPSH-----RPLKSPQ 293

DB 253 NNWYLSQGEATLTCDARSNPEPTGYNW-----STTMGLPLPPFAVQAQALLIRPVDKPI 306

QY 294 NET 296

DB 307 NTT 309

RESULT 6

JCS289

SHP substrate-1 protein, 513 - mouse

C|Species: Mus musculus (house mouse)

C|Date: 16-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004

C|Accession: JCS289

R|Yamano, T.; Matozaki, T.; Amano, K.; Marubuchi, Y.; Takahashi, N.; Ochi, F.; Fujioaka, Y.

Biochem Biophys Res Commun. 231, 61-67, 1997

A|Title: Mouse and human SHP-1 Molecular cloning of cDNAs and chromosomal localization

A|Reference number: JCS287; MUID:97223399; PMID:9070220

A|Content: Bzrain

A|Accession: JCS289

A|Molecule type: mRNA

A|Residues: 1-513 <YAM>

A|Cross-references: UNIPROT:P97797; DBJ:D87968; NID:g1864014; PIRN:BA13521.1; PIR:g1864014

C|Comment: This protein is a glycosylated receptor-like protein and plays a role in cellular acts as a docking protein and induce translocation of SHP-2 from the cytosol to the plasma membrane.

A|Gene: shp-1

A:Map position: 2

Query Match	7.3%	Score 115.5;	DB 2;	Length 513;
Best Local Similarity	22.3%;	Pred. No. 0.25;		
Matches	56;	Conservative 46;	Mismatches 84;	Indels 65; Gaps 13;
Oy	56 YYPWELATAPDVARISRRGHFGHQSFPSTRPSPHHKRYNRLFLNMWEGQSGFLRISNL 115	: :	:: :	:: :
Db	279 FXP-----EDQLIWL---NGNSRNDTPKKLTKN-----TDGYNTYSLFVNSSA 323	::	:: :	:: :
Oy	116 OKODSVFCRVLELDPRSSGRQOQSIEGFKLSITQAIVTTTTPQRPSMTTWRLSSTYT 175	::	:: :	:: :
Db	324 HRED-VVFFCCQGVHD-----QQ-----PATRN-----HYVLGLAHSSDQ 357	:	:: :	:: :
Oy	176 TGLRYTGKRSDSWHSIETAVGAVAVTVLGMILGLICLLMRRRKGQORTKATPPA 235	::	:: :	:: :
Db	358 GSMQGFPGNNATHNNMV----FIGVGACALLVLIMAAVLYLRHKQKAKGSTST-- 410	:	:: :	:: :
Oy	236 REPTPTEEPYEIR--NEGQNTDPKLNPPDDGIIVASIAL--SSSTSPRAPSPHRPLKS 291	::	:: :	:: :
Db	411 -----RIHPKKARREITQVSIIQDTNDIND-ITYADLNPKEKKAPRAP-----E 457	:	:: :	:: :
Oy	292 PONEFLSYLK 302			
Db	458 PNNHTEYSIE 468			

RESULT 7
RMHUPD
poliovirus receptor splice form delta precursor - human
N:Alternate names: poliovirus receptor #20B
C:Species: Homo sapiens (man)
C>Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C:Accession: A43024, B31496
R:Koike, S.; Horie, H.; Ise, I.; Okitsu, A.; Yoshida, M.; Itzuka, N.; Takeuchi, K.; Takeuchi, U., 9, 3217-3224, 1990
Article: The poliovirus receptor protein is produced both as membrane-bound and secreted
A:Reference number: S12048; MOID:91006015; PMID:2170108
A:Accession: A43024
A:Molecule type: DNA
A:Residues: 1-392 <KOI>
A:Cross-references: UNIPROT:P15151; EMBL:X64116
A>Note: 67-Ala was also found.
R:Mendelsohn, C.L.; Wimmer, E.; Racanietello, V.R.
Cell 56, 855-865, 1989
Article: Cellular receptor for poliovirus: molecular cloning, nucleotide sequence, and e
A:Reference number: A90910; MOID:89168426; PMID:2558245
A:Accession: B31496
A:Molecule type: mRNA
A:Residues: 1-66,'A','68-392 <MEN>
A:Cross-references: GB:M24406
C:Comment: The normal function of this receptor is unknown. Membrane-bound and soluble f
C:Genetics:
A:Gene: GDB:PVR; PVS
A:Cross-references: GDB:120324; OMIM:173850
A:Map position: 19q13.2-19q13.2
A:Introns: 27/1; 143/1; 242/1; 281/2; 331/1
C:Superfamily: poliovirus receptor; immunoglobulin homology
C:Keywords: alternative splicing; duplication; glycoprotein; receptor; transmembrane prot
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-392/Product: poliovirus receptor delta #status predicted <MRT>
F:21-392/Domain: extracellular #status predicted <EXT>
F:42-125/Domain: immunoglobulin homology <IM1>
F:159-223/Domain: immunoglobulin homology <IM2>
F:259-314/Domain: immunoglobulin homology <IM3>
F:344-367/Domain: transmembrane #status predicted <TMN>
F:368-392/Domain: intracellular #status predicted <INT>
F:49-123,166-221,266-312/Dsulfide bonds: #status predicted
F:105,120,189,218,237,278,307,313/Binding site: carbohydrate (Asn) (covalent) #status pr

C>Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S25758
R/Combiatco, G.; Kiobeck, H.G.
Bur. J. Immunol. 21, 1513-1522, 1991
A>Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam
A/Reference number: S16439; MUID:91257162; PMID:1904362
A/Accession: S25758
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-235 <COM>
A/Cross-References: EMBL:X57823; NID:g33745; PIDN:CAA0960.1; PID:g33746
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F:150-218/Domain: immunoglobulin homology <IMV>

Query Match 6.9%; Score 110; DB 2; Length 235;
Best Local Similarity 24.2%; Pred. No. 0.27;
Matches 48; Conservative 28; Mismatches 70; Indels 52; Gaps 8;

QY 26 GSGPSVLYGVTPKHLASMGGSVEIPFSFYYPWELATAPDVRISMGRGHFGSGFYSTR 85
DB 14 GTGSAQASALTGPASVSGSPGQSTITICT-----GSSSDV-----GGYVVSWMYQOH 60
QY 86 PSIIK-----DYVNRLL--FLNWTGQKSG---FLRISNQKODQSVYFCRVELDTRSSGR 136
DB 61 PKAPRLMIVDYTNRRSGVSNRFSGSKSGNTASLTISGLQPEADYIC-----TSKTS 115
QY 137 QQMOSIEGKLSI---TQAVTTTTPRSS-----MTTWRLSS 171
DB 116 SFYVEGTGTVKSVLGGPKANPTVTLFPFSESELQANKATVCLISDFYGAVTAMKADG 175
QY 172 TTTTGLARTQGRKRS 189
DB 176 SPVKAGVETTPSKQSN 193

RESULT 11
JH0371
B-cell adhesion protein CD22 beta splice form precursor - human
N/Alternate names: B-cell membrane protein CD22
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
A/Accession: JH0371; 156171
R/Wilson, G.L.; Fox, C.H.; Fauci, A.S.; Kehrl, J.H.
J. Exp. Med. 173, 137-146, 1991
A>Title: cDNA cloning of the B cell membrane protein CD22: a mediator of B-B cell intera
A/Reference number: JH0371; MUID:91086838; PMID:1985119
A/Accession: JH0371
A/Molecule type: mRNA
A/Residues: 1-847 <WIL>
A/Cross-References: UNIPROT:O60926; GB:X59350; NID:g36090; PIDN:CAA42006.1; PID:g36091
A/Experimental source: B lymphocyte
A/Note: the authors translated the codon AAT for residue 358 as Met
R/Wilson, G.L.; Najfeld, V.; Kozlow, E.; Weminger, J.; Ward, D.; Kehrl, J.H.
J. Immunol. 150, 5013-5024, 1993
A>Title: Genomic structure and chromosome mapping of the human CD22 gene.
A/Reference number: 156171; MUID:93267103; PMID:8496602
A/Accession: 156171
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 121-269, 'T', 271-473, 'K', 475-614, 'R', 616-638, 'Y', 640-711, 777-847 <WIL>
A/Cross-References: GB:S61375; NID:g385980; PIDN:AAIC18956.1; PID:g3184492
C/Genetic: GDB:CD22
A/Map position: 19q13.1-19q13.1
A/Introns: 138/1; 240/1; 329/1; 417/1; 503/1; 591/1; 679/1; 711/2; 804/3
C/Keywords: alternative splicing; B-cell; cell adhesion; dimer; glycoprotein; phosphoproc
F:1-19/Domain: signal sequence #status predicted <SID>
F:20-847/Product: B lymphocyte cell adhesion protein #status predicted <MAT>
F:346-398/Domain: immunoglobulin homology <IMM1>
F:609-661/Domain: immunoglobulin homology <IMM2>
F:688-706/Domain: transmembrane #status predicted <TMA>

F:67,101,112,135,164,231,363,445,448,479,574,634/Binding site: carbohydrate (Asn) (coval
F:764,789/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 6.9%; Score 110; DB 2; Length 847;
Best Local Similarity 22.1%; Pred. No. 1.2;
Matches 63; Conservative 40; Mismatches 116; Indels 66; Gaps 10;

QY 30 SYLYGVTPKHLASMGGSVEIPFSFYYPWELATAPDVRISMGRGH--FHGQFYST--- 84
DB 568 SYSCWVNSISQOTASKAWTLEV---LVAPRL-----RVSMSPEDQVMEGSAITLCE 618
QY 85 --RPSIIKDYVNRLEFLNWTGQKSGFRLINLQKODQSVYFCRVELDTRSSGQOMOSI 142
DB 619 DANPVSHTYTFD--WNNQSLPHHSQKRLRPVKVQSHGAIWQC---CTNSVKGK--- 669
QY 143 EGTKLSITQAVTTTTPRSSMTTWRLSSTTTTGLRVTQGRKRSDSWHISLETAIVGAV 202
DB 670 -----SPLSTLVYSSPETIGRAV-----AVGIGS 694
QY 203 AVTVYGMILGLCLRWRRRKQGRKATTPAREPQNTPEEPYENIRNEGQNDPKLNP 262
DB 695 CLAILILALIGLQRRKRTQSQGLQENSSGGSFFVRNKKVRRAPLSEBPHSLGCYNP 754
QY 263 -KDDGIVVASLASSTSPR-----APSHRPLKSPQNETLYSVL 301
DB 755 MMEGDSITTYTLRPFEMNIPRTGDAESSEMQRPRRTCDTVYTSAL 799

RESULT 12
S25747
Ig lambda chain - human
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S25747
R/Combiatco, G.; Kiobeck, H.G.
Bur. J. Immunol. 21, 1513-1522, 1991
A>Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam
A/Reference number: S16439; MUID:91257162; PMID:1904362
A/Accession: S25747
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-233 <COM>
A/Cross-References: EMBL:X57812; NID:g33723; PIDN:CAA0949.1; PID:g33724
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F:148-216/Domain: immunoglobulin homology <IMV>

Query Match 6.9%; Score 109.5; DB 2; Length 233;
Best Local Similarity 23.0%; Pred. No. 0.29;
Matches 53; Conservative 29; Mismatches 59; Indels 89; Gaps 11;

QY 5 LILPLPLLPAPLQPSGSGPSYLYGVTPKHLASMGGSVEIPFSFYYPWELATA 64
DB 6 LILGLL-----SHCTGSVTSYV--LTQPPSVAVARGKARI-----TC 41
QY 65 PDVRISMGRGHFGQS-----FY--STPPSHHDYVNRLLFNWTGQKSG---FLR 111
DB 42 GGINIASKSVHWYQKPKQAPVLVYGDSDPSGIPERF-----SGSNSGNTATLN 92
QY 112 ISNLQKODQSVYFCRVELDTRSSGQOMQSI-----GTRKLSI---TQAVTTTTPR 160
DB 93 ISRYEAGDEAAVYCOV-----WDSSSDHIVREGGKTLVYLGQPKAAPSTVTLFP 141
QY 161 SS-----MTTWRLSSTTTTGLRVTQGRKRS 189
DB 142 SSELQANKATVCLISDFYGAVTAMKADSPVKAGVETTPSKQSN 191

RESULT 13
S49449
Ig lambda chain - duck
C/Species: Anas platyrhynchos (domestic duck)
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000

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OM protein - protein search, using sw model

Run on: June 1, 2005, 22:02:25 ; Search time 43 seconds
(without alignments)
526.015 Million cell updates/sec

Title: US-10-777-524-2

Perfect score: 1591

Sequence: 1 MGRPLRLPLRLPLPAFLQ.....PSHRPLKSPQNETLYSVLKA 303

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCUTS.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1591	100.0	303	US-08-985-950-2	Sequence 2, Appli
2	1591	100.0	303	US-09-546-049-2	Sequence 2, Appli
3	1591	100.0	303	US-09-869-388-2	Sequence 2, Appli
4	1176.5	73.9	230	US-09-869-388-4	Sequence 4, Appli
5	973.5	61.2	226	US-09-869-388-10	Sequence 10, Appli
6	958	60.2	227	US-09-869-388-6	Sequence 6, Appli
7	934	58.7	238	US-09-149-476-485	Sequence 485, App
8	821	51.6	175	US-09-869-388-8	Sequence 8, Appli
9	517	32.5	101	US-09-149-476-754	Sequence 754, App
10	222	14.0	99	US-08-985-950-4	Sequence 4, Appli
11	222	14.0	99	US-09-546-049-4	Sequence 4, Appli
12	130.5	8.2	431	US-09-038-832-2	Sequence 2, Appli
13	130.5	8.2	431	US-09-038-832-4	Sequence 4, Appli
14	130.5	8.2	447	US-09-949-016-811	Sequence 811, Ap
15	119	7.5	341	US-09-336-536-29	Sequence 29, Appli
16	119	7.5	370	US-09-336-536-28	Sequence 28, Appli
17	114	7.2	390	US-08-979-424-1	Sequence 1, Appli
18	114	7.2	390	US-09-907-794A-39	Sequence 39, Appli
19	114	7.2	390	US-09-905-125A-39	Sequence 39, Appli
20	114	7.2	390	US-09-902-775A-39	Sequence 39, Appli
21	114	7.2	390	US-09-906-700-39	Sequence 39, Appli
22	114	7.2	390	US-09-903-603A-39	Sequence 39, Appli
23	114	7.2	390	US-09-904-920A-39	Sequence 39, Appli
24	114	7.2	390	US-09-909-064-39	Sequence 39, Appli
25	114	7.2	390	US-09-905-381A-39	Sequence 39, Appli
26	114	7.2	390	US-09-906-618-39	Sequence 39, Appli
27	114	7.2	417	US-09-949-016-6729	Sequence 6729, Ap

28	114	7.2	456	4	US-09-949-016-7564	Sequence 7564, Ap
29	113.5	7.1	319	1	US-08-597-495B-22	Sequence 22, Appli
30	113.5	7.1	319	3	US-09-066-051A-22	Sequence 22, Appli
31	113.5	7.1	319	4	US-09-336-536-67	Sequence 67, Appli
32	113.5	7.1	319	4	US-09-254-465A-6	Sequence 6, Appli
33	113.5	7.1	319	4	US-09-953-499-6	Sequence 6, Appli
34	113	7.1	316	4	US-09-397-243D-13	Sequence 13, Appli
35	111.5	7.0	306	4	US-09-369-247-63	Sequence 63, Appli
36	110.5	6.9	244	3	US-08-918-148-79	Sequence 79, Appli
37	110.5	6.9	244	4	US-09-138-051A-77	Sequence 77, Appli
38	110	6.9	300	2	US-08-661-052-4	Sequence 4, Appli
39	110	6.9	300	3	US-09-188-082-4	Sequence 4, Appli
40	110	6.9	300	3	US-09-364-088-4	Sequence 4, Appli
41	110	6.9	300	3	US-09-102-716-4	Sequence 4, Appli
42	110	6.9	501	2	US-08-408-095-31	Sequence 31, Appli
43	106.5	6.7	216	4	US-09-291-299A-9	Sequence 9, Appli
44	106.5	6.7	240	3	US-09-049-672A-11	Sequence 11, Appli
45	105	6.6	512	4	US-08-999-689A-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-08-985-950-2
Sequence 2, Application US/08985950
Patent No. 6140076
GENERAL INFORMATION:
APPLICANT: Adema, Gosse Jan
TITLE OF INVENTION: Isolated Mammalian Monocyte Cell Genes;
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSER: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,950
FILING DATE: 05-DEC-1997
CLASSIFICATION: 435
Prior Application DATA:
APPLICATION NUMBER: US 60/041,279
FILING DATE: 21-MARCH-1997
Prior Application DATA:
APPLICATION NUMBER: US 60/033,181
FILING DATE: 16-DEC-1996
Prior Application DATA:
APPLICATION NUMBER: US 60/032,252
FILING DATE: 06-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0670K
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEFAX: (650)496-1204
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 303 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-985-950-2
Query Match 100.0%; Score 1591; DB 3; Length 303;
Best Local Similarity 100.0%; Pred. No. 1.9e-141;

Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGRPLLLPLPLPLPAFLQPSGSGSYLYGVTPQPKHLASMGSGVEIPPSFYYPWE 60
DB 1 MGRPLLLPLPLPLPAFLQPSGSGSYLYGVTPQPKHLASMGSGVEIPPSFYYPWE 60

QY 61 LATAPDVRIISWRGHHFGHGSFYSTRPPIHKDYVNRFLFNMTEGOKSGFLRISNLOKODQ 120
DB 61 LATAPDVRIISWRGHHFGHGSFYSTRPPIHKDYVNRFLFNMTEGOKSGFLRISNLOKODQ 120

QY 121 SYVFCRVELDTRSSGROQWOSIEGTLSITQAVTTTQRPSSMTTWRLSSTTTTGLRV 180
DB 121 SYVFCRVELDTRSSGROQWOSIEGTLSITQAVTTTQRPSSMTTWRLSSTTTTGLRV 180

QY 181 TOGKRSDSMHISLETAVGAVAVATVGLIMILGICLLRMRRKGOQRTKATTPAREPQ 240
DB 181 TOGKRSDSMHISLETAVGAVAVATVGLIMILGICLLRMRRKGOQRTKATTPAREPQ 240

QY 241 NTEEPYENIRNEGQNTDPKLNPKDDGIVYASIALSSSTSPRAPPSHRPLKSPQNETLYSV 300
DB 241 NTEEPYENIRNEGQNTDPKLNPKDDGIVYASIALSSSTSPRAPPSHRPLKSPQNETLYSV 300

QY 301 LKA 303
DB 301 LKA 303

RESULT 2
US-09-546-049-2
Sequence 2, Application US/09546049
Patent No. 6479638
GENERAL INFORMATION:
APPLICANT: Adema, Gorge Jan
Meyard, Linde
Gorman, Daniel M.
McClanahan, Terrill K.
Zurawski, Sandra M.
Zurawski, Gerard
Lanier, Lewis L.
Phillips Jr., Joseph H.
TITLE OF INVENTION: Isolated Mammalian Monocyte Cell Genes;
Related Reagents
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESSES:
ADDRESSEE: DMAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/546,049
FILING DATE: 10-Apr-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/985,950
FILING DATE: 05-DEC-1997
APPLICATION NUMBER: US 60/041,279
FILING DATE: 21-MARCH-1997
APPLICATION NUMBER: US 60/033,181
FILING DATE: 16-DEC-1996
APPLICATION NUMBER: US 60/032,252
FILING DATE: 06-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0670K
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 852-9196

TELEFAX: (650) 496-1204
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 303 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-546-049-2

Query Match 100.0%; Score 1591; DB 4; Length 303;
Best Local Similarity 100.0%; Pred. No. 1.9e-141;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGRPLLLPLPLPLPAFLQPSGSGSYLYGVTPQPKHLASMGSGVEIPPSFYYPWE 60
DB 1 MGRPLLLPLPLPLPAFLQPSGSGSYLYGVTPQPKHLASMGSGVEIPPSFYYPWE 60

QY 61 LATAPDVRIISWRGHHFGHGSFYSTRPPIHKDYVNRFLFNMTEGOKSGFLRISNLOKODQ 120
DB 61 LATAPDVRIISWRGHHFGHGSFYSTRPPIHKDYVNRFLFNMTEGOKSGFLRISNLOKODQ 120

QY 121 SYVFCRVELDTRSSGROQWOSIEGTLSITQAVTTTQRPSSMTTWRLSSTTTTGLRV 180
DB 121 SYVFCRVELDTRSSGROQWOSIEGTLSITQAVTTTQRPSSMTTWRLSSTTTTGLRV 180

QY 181 TOGKRSDSMHISLETAVGAVAVATVGLIMILGICLLRMRRKGOQRTKATTPAREPQ 240
DB 181 TOGKRSDSMHISLETAVGAVAVATVGLIMILGICLLRMRRKGOQRTKATTPAREPQ 240

QY 241 NTEEPYENIRNEGQNTDPKLNPKDDGIVYASIALSSSTSPRAPPSHRPLKSPQNETLYSV 300
DB 241 NTEEPYENIRNEGQNTDPKLNPKDDGIVYASIALSSSTSPRAPPSHRPLKSPQNETLYSV 300

QY 301 LKA 303
DB 301 LKA 303

RESULT 3
US-09-869-388-2
Sequence 2, Application US/09869388
Patent No. 6774214
GENERAL INFORMATION:
APPLICANT: Bates, Elizabeth
APPLICANT: Chalus, Lionel
APPLICANT: Gattone, Pierre
APPLICANT: Pournier, Nathalie
TITLE OF INVENTION: MONOCYTE-DERIVED NUCLEIC ACIDS AND RELATED COMPOSITIONS AND METHOD
FILE REFERENCE: SF0977X
CURRENT APPLICATION NUMBER: US/09/869,388
CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: IBM PC compatible
SEQ ID NO 2
LENGTH: 303
TYPE: PRT
ORGANISM: homo sapiens
US-09-869-388-2

Query Match 100.0%; Score 1591; DB 4; Length 303;
Best Local Similarity 100.0%; Pred. No. 1.9e-141;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGRPLLLPLPLPLPAFLQPSGSGSYLYGVTPQPKHLASMGSGVEIPPSFYYPWE 60
DB 1 MGRPLLLPLPLPLPAFLQPSGSGSYLYGVTPQPKHLASMGSGVEIPPSFYYPWE 60

QY 61 LATAPDVRIISWRGHHFGHGSFYSTRPPIHKDYVNRFLFNMTEGOKSGFLRISNLOKODQ 120
DB 61 LATAPDVRIISWRGHHFGHGSFYSTRPPIHKDYVNRFLFNMTEGOKSGFLRISNLOKODQ 120

QY 121 SYVFCRVELDTRSSGROQWOSIEGTLSITQAVTTTQRPSSMTTWRLSSTTTTGLRV 180
DB 121 SYVFCRVELDTRSSGROQWOSIEGTLSITQAVTTTQRPSSMTTWRLSSTTTTGLRV 180

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Db      121 SVYFCRVELDTRSSGRQOMOSIEGKLSITQAVTTTQRPSSMTTWLSTTTTGLRV 180
Qy      181 TQGRKRSWSMHSLETAAGVAVAVTLGIMIGLICLLRMRRKQOQRTKATTPAREPQ 240
Db      181 TQGRKRSWSMHSLETAAGVAVAVTLGIMIGLICLLRMRRKQOQRTKATTPAREPQ 240
Qy      241 NTEBYENIRNEGONTDPKLNPKDGIYVASLALSSSTSPRAPSHRLKSPQNETLYSV 300
Db      241 NTEBYENIRNEGONTDPKLNPKDGIYVASLALSSSTSPRAPSHRLKSPQNETLYSV 300
Qy      301 LKA 303
Db      301 LKA 303

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RESULT 4
US-09-869-388-4
Sequence 4, Application US/09869388
Patent No. 6774214

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GENERAL INFORMATION:
APPLICANT: Bates, Elizabeth
APPLICANT: Fournier, Nathalie
APPLICANT: Chalus, Lionel
APPLICANT: Garrone, Pierre
TITLE OF INVENTION: MONOCYTE-DERIVED NUCLEIC ACIDS AND RELATED COMPOSITIONS AND METHO
FILE REFERENCE: SF0977X
CURRENT APPLICATION NUMBER: US/09/869,388
CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: IBM PC compatible
SEQ ID NO: 4
LENGTH: 230
TYPE: PRT
ORGANISM: homo sapiens
US-09-869-388-4

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Query Match 73.9%; Score 1176.5; DB 4; Length 230;
Best Local Similarity 75.9%; Pred. No. 1.2e-102;
Matches 230; Conservative 0; Mismatches 0; Indels 73; Gaps 1;

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Qy      1 MGRPLLLPLPLLPAPFLOPSGSGSPSYLVGVTOPKHLASMGSGVEIPFSFYPMW 60
Db      1 MGRPLLLPLPLLPAPFLOPSGSGSPSYLVGVTOPKHLASMGSGVEIPFSFYPMW 60
Qy      61 LATAPDVIRISWRGHFHGQSFYSTRPSIHKDYVNRFLNMTGQSGFLRISNLQKQDQ 120
Db      61 LATAPDVIRISWRGHFHGQSFYSTRPSIHKDYVNRFLNMTGQSGFLRISNLQKQDQ 120
Qy      121 SVYFCRVELDTRSSGRQOMOSIEGKLSITQAVTTTQRPSSMTTWLSTTTTGLRV 180
Db      121 SVYFCRVELDTRSSGRQOMOSIEGKLSITQAVTTTQRPSSMTTWLSTTTTGLRV 180
Qy      181 TQGRKRSWSMHSLETAAGVAVAVTLGIMIGLICLLRMRRKQOQRTKATTPAREPQ 240
Db      181 TQGRKRSWSMHSLETAAGVAVAVTLGIMIGLICLLRMRRKQOQRTKATTPAREPQ 240
Qy      241 NTEBYENIRNEGONTDPKLNPKDGIYVASLALSSSTSPRAPSHRLKSPQNETLYSV 300
Db      241 NTEBYENIRNEGONTDPKLNPKDGIYVASLALSSSTSPRAPSHRLKSPQNETLYSV 300
Qy      301 LKA 303
Db      301 LKA 303

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RESULT 5
US-09-869-388-10
Sequence 10, Application US/09869388
Patent No. 6774214
GENERAL INFORMATION:
APPLICANT: Bates, Elizabeth
APPLICANT: Fournier, Nathalie

```

APPLICANT: Chalus, Lionel
APPLICANT: Garrone, Pierre
TITLE OF INVENTION: MONOCYTE-DERIVED NUCLEIC ACIDS AND RELATED COMPOSITIONS AND METHO
FILE REFERENCE: SF0977X
CURRENT APPLICATION NUMBER: US/09/869,388
CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: IBM PC compatible
SEQ ID NO: 10
LENGTH: 226
TYPE: PRT
ORGANISM: homo sapiens
US-09-869-388-10

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Query Match 61.2%; Score 973.5; DB 4; Length 226;
Best Local Similarity 82.5%; Pred. No. 1.5e-83;
Matches 188; Conservative 14; Mismatches 17; Indels 9; Gaps 2;

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Qy      1 MGRPLLLPLPLLPAPFLOPSGSGSPSYLVGVTOPKHLASMGSGVEIPFSFYPMW 60
Db      1 MGRPLLLPLPLLPAPFLOPSGSGSPSYLVGVTOPKHLASMGSGVEIPFSFYPMW 60
Qy      61 LATAPDVIRISWRGHFHGQSFYSTRPSIHKDYVNRFLNMTGQSGFLRISNLQKQDQ 120
Db      61 LATAPDVIRISWRGHFHGQSFYSTRPSIHKDYVNRFLNMTGQSGFLRISNLQKQDQ 120
Qy      121 SVYFCRVELDTRSSGRQOMOSIEGKLSITQAVTTTQRPSSMTTWLSTTTTGLRV 180
Db      121 SVYFCRVELDTRSSGRQOMOSIEGKLSITQAVTTTQRPSSMTTWLSTTTTGLRV 180
Qy      181 TQGRKRSWSMHSLETAAGVAVAVTLGIMIGLICLLRMRRKQOQRTKATTPAREPQ 240
Db      181 TQGRKRSWSMHSLETAAGVAVAVTLGIMIGLICLLRMRRKQOQRTKATTPAREPQ 240

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RESULT 6
US-09-869-388-6
Sequence 6, Application US/09869388
Patent No. 6774214

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GENERAL INFORMATION:
APPLICANT: Bates, Elizabeth
APPLICANT: Fournier, Nathalie
APPLICANT: Chalus, Lionel
APPLICANT: Garrone, Pierre
TITLE OF INVENTION: MONOCYTE-DERIVED NUCLEIC ACIDS AND RELATED COMPOSITIONS AND METHO
FILE REFERENCE: SF0977X
CURRENT APPLICATION NUMBER: US/09/869,388
CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: IBM PC compatible
SEQ ID NO: 6
LENGTH: 227
TYPE: PRT
ORGANISM: homo sapiens
US-09-869-388-6

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Query Match 60.2%; Score 958; DB 4; Length 227;
Best Local Similarity 80.8%; Pred. No. 4.2e-82;
Matches 185; Conservative 15; Mismatches 19; Indels 10; Gaps 2;

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Qy      1 MGRPLLLPLPLLPAPFLOPSGSGSPSYLVGVTOPKHLASMGSGVEIPFSFYPMW 60
Db      1 MGRPLLLPLPLLPAPFLOPSGSGSPSYLVGVTOPKHLASMGSGVEIPFSFYPMW 60
Qy      61 LATAPDVIRISWRGHFHGQSFYSTRPSIHKDYVNRFLNMTGQSGFLRISNLQKQDQ 120
Db      61 LATAPDVIRISWRGHFHGQSFYSTRPSIHKDYVNRFLNMTGQSGFLRISNLQKQDQ 120
Qy      121 SVYFCRVELDTRSSGRQOMOSIEGKLSITQAVTTTQRPSSMTTWLSTTTTGLRV 180
Db      121 SVYFCRVELDTRSSGRQOMOSIEGKLSITQAVTTTQRPSSMTTWLSTTTTGLRV 180
Qy      181 TQGRKRSWSMHSLETAAGVAVAVTLGIMIGLICLLRMRRKQOQRTKATTPAREPQ 240
Db      181 TQGRKRSWSMHSLETAAGVAVAVTLGIMIGLICLLRMRRKQOQRTKATTPAREPQ 240

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Db 173 TESGHSWHLSDTAIRVALAVAVKTVILGLCULLMWRKGR 221

RESULT 7
US-09-149-476-485
Sequence 485, Application US/09149476
Patent No. 6420526
GENERAL INFORMATION:
APPLICANT: Roehen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: P202P1
CURRENT APPLICATION NUMBER: US/09/149, 476
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040, 162
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040, 333
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/038, 621
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040, 626
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040, 334
EARLIER FILING DATE: 1997-03-07
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EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040, 163
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/047, 600
EARLIER FILING DATE: 1997-05-23
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EARLIER APPLICATION NUMBER: 60/047, 597
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047, 502
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047, 633
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EARLIER APPLICATION NUMBER: 60/047, 612
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047, 632
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EARLIER APPLICATION NUMBER: 60/047, 601

EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043, 580
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043, 568
EARLIER FILING DATE: 1997-04-11
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EARLIER APPLICATION NUMBER: 60/043, 311
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043, 671
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EARLIER APPLICATION NUMBER: 60/043, 315
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/048, 974
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/056, 886
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 877
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EARLIER FILING DATE: 1997-08-22
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EARLIER APPLICATION NUMBER: 60/056, 903
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EARLIER APPLICATION NUMBER: 60/056, 888
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EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056, 892
EARLIER FILING DATE: 1997-08-22

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; EARLIER APPLICATION NUMBER: 60/057,761
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/047,595
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,599
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,588
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; EARLIER APPLICATION NUMBER: 60/047,614
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; EARLIER APPLICATION NUMBER: 60/043,578
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; EARLIER APPLICATION NUMBER: 60/043,576
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; EARLIER APPLICATION NUMBER: 60/047,501
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,670
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; EARLIER APPLICATION NUMBER: 60/056,632
; EARLIER FILING DATE: 1997-08-22
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; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,881
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; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

Query Match      58.7%; Score 934; DB 4; Length 238;
Best Local Similarity 82.1%; Pred. No. 8, 2e-80;
Matches 179; Conservative 13; Mismatches 18; Indels 8; Gaps 1;
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Qy      121 SVFRCVELDTRSSGRQOMOSIEGKLSITQAVTTTTPRSPMTTTLRLSTTTTGLRV 180
        |||||
Db      121 SVFRCVELDTRRRGRQOLQSIKTKLTITQAVTT-----TTTWRPSTTTIAGLRV 172
Qy      181 TQKRKRSDSMHSLETAVGVAATVIGIMILGICLL 218
        |||||
Db      173 TESKHSSEMSLSDTATRALVALAVLKTIVILGLICLL 210

RESULT 8
US-09-869-388-8
; Sequence 8, Application US/09869388
; Patent No. 6774214
; GENERAL INFORMATION:
; APPLICANT: Bates, Elizabeth
; APPLICANT: Fournier, Nathalie
; APPLICANT: Chalus, Lionel
; APPLICANT: Garrone, Pierre
; TITLE OF INVENTION: MONOCYTE-DERIVED NUCLEIC ACIDS AND RELATED COMPOSITIONS AND METHO
; FILE REFERENCE: SP0977X
; CURRENT APPLICATION NUMBER: US/09/869,388
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: IBM PC compatible
; SEQ ID NO 8
; LENGTH: 175
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-869-388-8
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Query Match 51.6%; Score 821; DB 4; Length 175;
Best Local Similarity 96.9%; Pred. No. 2, 2e-69;
Matches 154; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

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Qy      1 MGRPLLPPLPPLPPAFLOPSGSGPSYLYGVTPQKHLASNGSGVEIPFSFYPMW 60
        |||||
Db      1 MGRPLLPPLPPLPPAFLOPSGSGPSYLYGVTPQKHLASNGSGVEIPFSFYPMW 60
Qy      61 LATAPDVRIWMRGHFGHGSFYSTRPPSIHKDYVNRFLFNMTEGQKSGFLRISNLQKODQ 120
        |||||
Db      61 LATAPDVRIWMRGHFGHGSFYSTRPPSIHKDYVNRFLFNMTEGQKSGFLRISNLQKODQ 120
Qy      121 SVFRCVELDTRSSGRQOMOSIEGKLSITQAVTTTTR 159
        |||||
Db      121 SVFRCVELDTRSSGRQOMOSIEGKLSITQGNPSKTOR 159

RESULT 9
US-09-149-476-754
; Sequence 754, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
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	EARLIER APPLICATION NUMBER: 60/047,600
1	EARLIER FILING DATE: 1997-05-23
2	EARLIER APPLICATION NUMBER: 60/047,615
3	EARLIER FILING DATE: 1997-05-23
4	EARLIER APPLICATION NUMBER: 60/047,597
5	EARLIER FILING DATE: 1997-05-23
6	EARLIER APPLICATION NUMBER: 60/047,502
7	EARLIER FILING DATE: 1997-05-23
8	EARLIER APPLICATION NUMBER: 60/047,633
9	EARLIER FILING DATE: 1997-05-23
10	EARLIER APPLICATION NUMBER: 60/047,583
11	EARLIER FILING DATE: 1997-05-23
12	EARLIER APPLICATION NUMBER: 60/047,617
13	EARLIER FILING DATE: 1997-05-23
14	EARLIER APPLICATION NUMBER: 60/047,618
15	EARLIER FILING DATE: 1997-05-23
16	EARLIER APPLICATION NUMBER: 60/047,503
17	EARLIER FILING DATE: 1997-05-23
18	EARLIER APPLICATION NUMBER: 60/047,592
19	EARLIER FILING DATE: 1997-05-23
20	EARLIER APPLICATION NUMBER: 60/047,581
21	EARLIER FILING DATE: 1997-05-23
22	EARLIER APPLICATION NUMBER: 60/047,584
23	EARLIER FILING DATE: 1997-05-23
24	EARLIER APPLICATION NUMBER: 60/047,500
25	EARLIER FILING DATE: 1997-05-23
26	EARLIER APPLICATION NUMBER: 60/047,587
27	EARLIER FILING DATE: 1997-05-23
28	EARLIER APPLICATION NUMBER: 60/047,492
29	EARLIER FILING DATE: 1997-05-23
30	EARLIER APPLICATION NUMBER: 60/047,598
31	EARLIER FILING DATE: 1997-05-23
32	EARLIER APPLICATION NUMBER: 60/047,613
33	EARLIER FILING DATE: 1997-05-23
34	EARLIER APPLICATION NUMBER: 60/047,582
35	EARLIER FILING DATE: 1997-05-23
36	EARLIER APPLICATION NUMBER: 60/047,596
37	EARLIER FILING DATE: 1997-05-23
38	EARLIER APPLICATION NUMBER: 60/047,612
39	EARLIER FILING DATE: 1997-05-23
40	EARLIER APPLICATION NUMBER: 60/047,632
41	EARLIER FILING DATE: 1997-05-23
42	EARLIER APPLICATION NUMBER: 60/047,601
43	EARLIER FILING DATE: 1997-05-23
44	EARLIER APPLICATION NUMBER: 60/043,580
45	EARLIER FILING DATE: 1997-04-11
46	EARLIER APPLICATION NUMBER: 60/043,568
47	EARLIER FILING DATE: 1997-04-11
48	EARLIER APPLICATION NUMBER: 60/043,314
49	EARLIER FILING DATE: 1997-04-11
50	EARLIER APPLICATION NUMBER: 60/043,569
51	EARLIER FILING DATE: 1997-04-11
52	EARLIER APPLICATION NUMBER: 60/043,311
53	EARLIER FILING DATE: 1997-04-11
54	EARLIER APPLICATION NUMBER: 60/043,671
55	EARLIER FILING DATE: 1997-04-11
56	EARLIER APPLICATION NUMBER: 60/043,674
57	EARLIER FILING DATE: 1997-04-11
58	EARLIER APPLICATION NUMBER: 60/043,669
59	EARLIER FILING DATE: 1997-04-11
60	EARLIER APPLICATION NUMBER: 60/043,312
61	EARLIER FILING DATE: 1997-04-11
62	EARLIER APPLICATION NUMBER: 60/043,313
63	EARLIER FILING DATE: 1997-04-11
64	EARLIER APPLICATION NUMBER: 60/043,672
65	EARLIER FILING DATE: 1997-04-11
66	EARLIER APPLICATION NUMBER: 60/043,315
67	EARLIER FILING DATE: 1997-04-11
68	EARLIER APPLICATION NUMBER: 60/048,974
69	EARLIER FILING DATE: 1997-06-06
70	EARLIER APPLICATION NUMBER: 60/056,886
71	EARLIER FILING DATE: 1997-08-22
72	EARLIER APPLICATION NUMBER: 60/056,877
73	EARLIER FILING DATE: 1997-08-22
74	EARLIER APPLICATION NUMBER: 60/056,889
75	EARLIER FILING DATE: 1997-08-22
76	EARLIER APPLICATION NUMBER: 60/056,893
77	EARLIER FILING DATE: 1997-08-22
78	EARLIER APPLICATION NUMBER: 60/056,630
79	EARLIER FILING DATE: 1997-08-22
80	EARLIER APPLICATION NUMBER: 60/056,878
81	EARLIER FILING DATE: 1997-08-22
82	EARLIER APPLICATION NUMBER: 60/056,662
83	EARLIER FILING DATE: 1997-08-22
84	EARLIER APPLICATION NUMBER: 60/056,872
85	EARLIER FILING DATE: 1997-08-22
86	EARLIER APPLICATION NUMBER: 60/056,882
87	EARLIER FILING DATE: 1997-08-22
88	EARLIER APPLICATION NUMBER: 60/056,888
89	EARLIER FILING DATE: 1997-08-22
90	EARLIER APPLICATION NUMBER: 60/056,879
91	EARLIER FILING DATE: 1997-08-22
92	EARLIER APPLICATION NUMBER: 60/056,880
93	EARLIER FILING DATE: 1997-08-22
94	EARLIER APPLICATION NUMBER: 60/056,894
95	EARLIER FILING DATE: 1997-08-22
96	EARLIER APPLICATION NUMBER: 60/056,911
97	EARLIER FILING DATE: 1997-08-22
98	EARLIER APPLICATION NUMBER: 60/056,636
99	EARLIER FILING DATE: 1997-08-22
100	EARLIER APPLICATION NUMBER: 60/056,874
101	EARLIER FILING DATE: 1997-08-22
102	EARLIER APPLICATION NUMBER: 60/056,910
103	EARLIER FILING DATE: 1997-08-22
104	EARLIER APPLICATION NUMBER: 60/056,864
105	EARLIER FILING DATE: 1997-08-22
106	EARLIER APPLICATION NUMBER: 60/056,631
107	EARLIER FILING DATE: 1997-08-22
108	EARLIER APPLICATION NUMBER: 60/056,845
109	EARLIER FILING DATE: 1997-08-22
110	EARLIER APPLICATION NUMBER: 60/056,892
111	EARLIER FILING DATE: 1997-08-22
112	EARLIER APPLICATION NUMBER: 60/057,761
113	EARLIER FILING DATE: 1997-08-22
114	EARLIER APPLICATION NUMBER: 60/047,595
115	EARLIER FILING DATE: 1997-05-23
116	EARLIER APPLICATION NUMBER: 60/047,586
117	EARLIER FILING DATE: 1997-05-23
118	EARLIER APPLICATION NUMBER: 60/047,589
119	EARLIER FILING DATE: 1997-05-23
120	EARLIER APPLICATION NUMBER: 60/047,590
121	EARLIER FILING DATE: 1997-05-23

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EARLIER APPLICATION NUMBER: 60/056,632
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,664
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,876
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,881
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,909
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,875
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,862
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,887
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,908
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/057,650
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056,884
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057,669
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02
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Query Match 32.5%; Score 517; DB 4; Length 101;

Best Local Similarity 93.1%; Pred. No. 4e-41; Matches 94; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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Oy 35 VTQPHLSASMGSGVEIPFSFYPMELATAPVRISMGRGHGOSFYSTRPPIHKDYV 94
Db 1 VTQPHLSASMGSGVEIPFSFYPMELATAPVRISMGRGHGOSFYSTRPPIHKDYV 60
Oy 95 NRLFLNMTGQKSGFLRISNLOKQDOSVYFCVVELDTRSSG 135
Db 61 NRLFLNMTGQKSGFLRISNLOKQDOSVYFCVVELDTRSSG 101
```

```
RESULT 10
US-08-985-950-4
Sequence 4, Application US/08985950
Patent No. 6140076
GENERAL INFORMATION:
APPLICANT: Adema, Gosee Jan
TITLE OF INVENTION: Isolated Mammalian Monocyte Cell Genes;
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESS: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,950
FILING DATE: 05-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/041,279
FILING DATE: 21-MARCH-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,181
```

```
FILING DATE: 16-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/032,252
FILING DATE: 06-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0670X
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEFAX: (650)496-1204
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-985-950-4
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Query Match 14.0%; Score 222; DB 3; Length 99;

Best Local Similarity 45.2%; Pred. No. 2.1e-13; Matches 42; Conservative 15; Mismatches 30; Indels 6; Gaps 1;

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Oy 19 LQPSGTSQSPSYL-----GVTPKHLASMGSGVEIPFSFYPMELATAPVRISMGR 72
Db 7 LSSGCLHAGNSERNRNGRGVNPGRSCGVGGSSIIIPFSFYPMELANDPQMSIAWK 66
Oy 73 RGHFHGSGFYSTRPPIHKDYVNLFLNMTGQ 105
Db 67 WDFHGEVIVNSLPIFHEHFKRLILNMTGQ 99
```

RESULT 11

US-09-546-049-4

Sequence 4, Application US/09546049

Patent No. 6479638

GENERAL INFORMATION:

APPLICANT: Adema, Gosee Jan

Meyard, Linde

Gorman, Daniel M.

McClanahan, Terrill K.

Zurawski, Sandra M.

Zurawski, Gerard

Lanier, Lewis L.

Phillips Jr., Joseph H.

TITLE OF INVENTION: Isolated Mammalian Monocyte Cell Genes;

Related Reagents

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESS: DNAX Research Institute

STREET: 901 California Avenue

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94304-1104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/546,049

FILING DATE: 10-APR-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/985,950

FILING DATE: 05-DEC-1997

APPLICATION NUMBER: US 60/041,279

FILING DATE: 21-MARCH-1997

APPLICATION NUMBER: US 60/033,181

FILING DATE: 16-DEC-1996

APPLICATION NUMBER: US 60/032,252

FILING DATE: 06-DEC-1996

ATTORNEY/AGENT INFORMATION:

NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0670X
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEFAX: (650)496-1204
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
-US-09-546-049-4

Query Match 14.0%; Score 222; DB 4; Length 99;
Best Local Similarity 45.2%; Pred. No. 2,1e-13;
Matches 42; Conservative 15; Mismatches 30; Indels 6; Gaps 1;

Qy 19 LQPSGSGSGPSYLY-----GVTPKHLASMGSGVEIPSFYPMELATAPDPRISWR 72
Db 7 LLSGCLHAGNSERYNKRNGRVQVQPERCSGVGSGSIDIPSFYPMKLAKDPQMSIAWK 66

Qy 73 RGHFGSGFYSTRPSPSIHKDYVNLFLNWTGQ 105
Db 67 WKDFHGEIVYNSLPFIHEHPKGRLLINWTGQ 99

RESULT 12
US-09-038-832-2
Sequence 2, Application US/09038832
Patent No. 6146845
GENERAL INFORMATION:
APPLICANT: KIKLY, KRISTINE
APPLICANT: ERICKSON-MILLER, CONNIE
TITLE OF INVENTION: Sialoadhesin Family Member-2
TITLE OF INVENTION: (SAF-2)
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: RATNER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/038,832
FILING DATE: 11-MAR-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/041,886
FILING DATE: 02-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-50018
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 431 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-038-832-2

Query Match 8.2%; Score 130.5; DB 3; Length 431;
Best Local Similarity 22.6%; Pred. No. 0.00067;
Matches 83; Conservative 45; Mismatches 138; Indels 101; Gaps 14;

Qy 5 LLLPLPLLPAPLQPSGSGSPSYLYGVTPKHLASMGSGVEIPSFYPMELATA 64
Db 3 LLLLLPLLMGTGKME--GDRQGDGYLLQVQE--LVTVQEGICVAVPCSFSPQGWTD 58

Qy 65 PD-VRIWRGRHFGSGFYSTRPSPSIHKDYVNLFLNWTGQ-----XSGFLRISN 114
Db 59 SDPVHGYWFRPA--GDRPYQDAPVATNMP--PREVOAEYQGRQLGDIWSDCSLSIRD 113

Qy 115 LOKODSVYFCRYE-----LDTRSSGRCQ-- 138
Db 114 ARGRDGSYFFRLERSMCKSYKSQNLTKQLSVFTALTHRPDLILIGTSGHSRNL 173

Qy 139 ----WQSIETKLSIT-----QAVTTTQRPBSMTTWRLSITTTTGL 178
Db 174 TCSVPACKQGFPPMISWIGASVSPGPTTARSSVLTLPKPDHGTSLTCQVTLPGTV 233

Qy 179 RYVQGRBDS--WHISL-----ETAVGVANAVTVLGIMIGLCL-----L 218
Db 234 TTTSTVRLVSYPPMNLTWVFOGDATASTALGNGSSLSLVESQSLRLVCVANSPPARL 293

Qy 219 RWRRRGQORTATTPAREPFQV--TEEPYENIRNEGQNTDPKLNPDQDIIVYASIALSS 277
Db 294 SWTR-----GSLTLCPSRSSNPGLLEPRVHVRDBGEFTCRQNMAGSGHISLSLQNE 348

Qy 278 TSPRAPP 284
Db 349 GTGTSRP 355

RESULT 13
US-09-038-832-4
Sequence 4, Application US/09038832
Patent No. 6146845
GENERAL INFORMATION:
APPLICANT: KIKLY, KRISTINE
APPLICANT: ERICKSON-MILLER, CONNIE
TITLE OF INVENTION: Sialoadhesin Family Member-2
TITLE OF INVENTION: (SAF-2)
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: RATNER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/038,832
FILING DATE: 11-MAR-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/041,886
FILING DATE: 02-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-50018
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:

LENGTH: 431 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-038-832-4

Query Match 8.2%; Score 130.5; DB 3; Length 431;
Best Local Similarity 22.6%; Pred. No. 0.00067;
Matches 83; Conservative 45; Mismatches 138; Indels 101; Gaps 14;

QY LLLPLPLPLPPAFLOPSGSGTSGPSYLYGVYTOPKHLASMGSGVEIPFSFYPMELATA 64
DB LLLPLPLPLMTGKME---GDRYGDGYLLQVQE--LVTVQBELCYHVCFSFYPODGMTD 58
QY 65 PD-VRISWRGHFHGQSFYSTRPSIHKDVNRLFLNMTGQ-----KSGFLRISN 114
DB 59 SDPVHGYWFR---GDRPYQAPVATNPN--DREVQAEQGRFQLLDIWSNDCSLSRD 113
QY 115 LQKQDQSYVFCRVE-----LDRSSGRQ-- 138
DB 114 ARKDKGSGYFRLERSGMKMSYKQLNKTQKLSVFTALTHRPDILLGLTSGHSNRL 173
QY 139 ---WQIEGFKLSIT-----QAVTTTORPSSMTTWRLSSTTTTGL 178
DB 174 TCSVPMACKQGTTPPMISWIGASVSPGPTTARSSVLITPKQDHGTSITCQVTLPGTGV 233
QY 179 RVYQGRKRSDS---WHISL-----ETAVGVAVAVTVLIGMILGICL-----L 218
DB 234 TTTSTVRLDVSPYPMNLMTVTFQGDATASTALNGSSLSVLEGQSLRLVCVANSNPPARL 293
QY 219 RWRRRKQGRKATTPPAEPFQ--TEEPYENIRNEGQTDPKLNKQDGIYASIALSSS 277
DB 294 SWTR-----GSLTLCPSRSSNPGLELPRVHVHREGEFTCRAQNAQSGSHISLSLQNE 348
QY 278 TSPRAP 284
DB 349 GTGTSRP 355

RESULT 14
US-09-949-016-8211
Sequence 8211, Application US/09949016
Patent No. 6612339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 8211
LENGTH: 447
TYPE: PRT
ORGANISM: Human
US-09-949-016-8211

Query Match 8.2%; Score 130.5; DB 4; Length 447;
Best Local Similarity 22.6%; Pred. No. 0.00071;
Matches 83; Conservative 45; Mismatches 138; Indels 101; Gaps 14;
QY 5 LLLPLPLPLPPAFLOPSGSGTSGPSYLYGVYTOPKHLASMGSGVEIPFSFYPMELATA 64
DB 19 LLLPLPLPLMTGKME---GDRYGDGYLLQVQE--LVTVQBELCYHVCFSFYPODGMTD 74

QY 65 PD-VRISWRGHFHGQSFYSTRPSIHKDVNRLFLNMTGQ-----KSGFLRISN 114
DB 75 SDPVHGYWFR---GDRPYQAPVATNPN--DREVQAEQGRFQLLDIWSNDCSLSRD 129
QY 115 LQKQDQSYVFCRVE-----LDRSSGRQ-- 138
DB 130 ARKDKGSGYFRLERSGMKMSYKQLNKTQKLSVFTALTHRPDILLGLTSGHSNRL 189
QY 139 ---WQIEGFKLSIT-----QAVTTTORPSSMTTWRLSSTTTTGL 178
DB 190 TCSVPMACKQGTTPPMISWIGASVSPGPTTARSSVLITPKQDHGTSITCQVTLPGTGV 249
QY 179 RVYQGRKRSDS---WHISL-----ETAVGVAVAVTVLIGMILGICL-----L 218
DB 250 TTTSTVRLDVSPYPMNLMTVTFQGDATASTALNGSSLSVLEGQSLRLVCVANSNPPARL 309
QY 219 RWRRRKQGRKATTPPAEPFQ--TEEPYENIRNEGQTDPKLNKQDGIYASIALSSS 277
DB 310 SWTR-----GSLTLCPSRSSNPGLELPRVHVHREGEFTCRAQNAQSGSHISLSLQNE 364
QY 278 TSPRAP 284
DB 365 GTGTSRP 371

RESULT 15
US-09-336-536-29
Sequence 29, Application US/09336536
Patent No. 6406884
GENERAL INFORMATION:
APPLICANT: Leidy, K.
APPLICANT: McKay, C.
APPLICANT: Bossone, S.
TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
FILE REFERENCE: 7853-144
CURRENT APPLICATION NUMBER: US/09/336,536
CURRENT FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 29
LENGTH: 341
TYPE: PRT
ORGANISM: Mus musculus
US-09-336-536-29

Query Match 7.5%; Score 119; DB 4; Length 341;
Best Local Similarity 21.4%; Pred. No. 0.0058;
Matches 71; Conservative 44; Mismatches 127; Indels 90; Gaps 11;

QY 10 LPLPLPPAFLOPSGSGTSGPSYLYGVYTOPKHLASMGSGVEIPFSFYPMELATAPDVRI 69
DB 2 LQHLFANRLQAVEGEGSASAWYTL---HREVSSQPMVEVPVWVF--FKQKEKEDVL 56
QY 70 SWRGHFGHGSFYSTRPSIHKDVNRLFLNMTGQSGFLRISNLOKQDQSYVFCRVEL 129
DB 57 SYING-----VTSKRGVS-----LVYSMPRSRLSKRVGLQKDGSPYSCSYNV 101
QY 130 DTRSSGRQWQIEGFKLSIT-----QAVTTTORPSSMTTWRLSSTTTTGL 167
DB 102 QDK-QGKSRGHSITLLENLVPPAPRSCRLQGVPHGANVTLSCQSPRSKPAVQYQWDR 160
QY 168 -----RLSSTTTTGLRVYQGRKRSDSWHISLLETAVGVAVAV 204
DB 161 QLPSEFOTFFAPALDVINGSLTLYLSSMAGVVCANHEVGTACQCVTLLEVSTGPAAV 220
QY 205 -----TVLIGMILGICLWRRRKQGRKATTPPAEPFQTEEPYENIRNEGQTD 257
DB 221 VAEAVGTVLVLGLAGLIVLYHRRGA-----LEEPANDIKEDALAPR 264
QY 258 PKLNPKDGIYASIALSSSSTSPRA--PSSHAP 288
DB 265 TLPMPKSSDITISKNGITLSSVTSARALRPHHP 296

Thu Jun 2 12:31:25 2005

us-10-777-524-2.ra1

Page 10

Search completed: June 1, 2005, 22:14:50
Job time : 45 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 1, 2005, 22:00:25 ; Search time 173 Seconds

(without alignments)
896.879 Million cell updates/sec

Title: US-10-777-524-2

Perfect score: 1591

Sequence: 1 MGRPLLPPLLPPLPPAPLQ.....PSHRPLKSPQNETLYSVLKA 303

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_03:*

1: uniprot_03:*

2: uniprot_03:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1588	99.8	303	Q9UKJ1	Q9UKJ1 homo sapien
2	997.5	62.7	226	Q8NH11	Q8NH11 homo sapien
3	958	60.2	227	Q9UKJ0	Q9UKJ0 homo sapien
4	630	39.6	299	Q8BYA6	Q8BYA6 mus musculu
5	144.5	9.1	823	AXL2 YEAST	P38928 saccharomyc
6	139	8.7	290	Q6UX24	Q6UX24 homo sapien
7	139	8.7	290	Q7Z6A6	Q7Z6A6 homo sapien
8	136	8.5	290	Q8TDQ1	Q8TDQ1 homo sapien
9	135.5	8.5	293	Q7Z715	Q7Z715 homo sapien
10	130.5	8.2	499	SIL8 HUMAN	Q9NY24 homo sapien
11	130	8.1	289	Q6QX36	Q6QX36 mus musculu
12	129.5	8.1	233	Q8BHC9	Q8BHC9 homo sapien
13	129.5	8.1	499	Q7Z728	Q7Z728 homo sapien
14	123.5	7.8	328	Q6ZMC9	Q6ZMC9 homo sapien
15	123.5	7.8	353	Q7SDQ5	Q7SDQ5 homo sapien
16	122.5	7.7	235	Q9SM11	Q9SM11 mus musculu
17	122	7.7	288	Q46707	Q46707 fugu rubrip
18	122	7.7	288	Q6GJF4	Q6GJF4 fugu rubrip
19	120	7.5	236	Q6RI07	Q6RI07 homo sapien
20	119.5	7.5	434	Q872V2	Q872V2 neurospora
21	119	7.4	318	Q91B03	Q91B03 spheroeloides
22	117.5	7.4	235	Q6P2J1	Q6P2J1 homo sapien
23	117.5	7.4	366	Q46705	Q46705 fugu rubrip
24	116	7.3	417	PVR CERAE	P32506 cercopithec
25	115.5	7.3	513	SHS1 MOUSE	P97797 m. protein-t
26	115	7.2	367	Q46706	Q46706 fugu rubrip
27	114.5	7.2	235	Q6PUG0	Q6PUG0 homo sapien
28	114	7.2	390	Q96AP7	Q96AP7 homo sapien
29	114	7.2	390	Q96T50	Q96T50 homo sapien
30	114	7.2	417	PVR HUMAN	P15151 homo sapien
31	113.5	7.1	319	A33_HUMAN	Q99795 homo sapien

32	113.5	7.1	387	2	Q64JA4	Q64JA4 pan troglod
33	113	7.1	401	2	Q08835	Q08835 cercopithec
34	113	7.1	718	2	Q73675	Q73675 xenopus lae
35	113	7.1	718	2	Q6PCK4	Q6PCK4 xenopus lae
36	112.5	7.1	403	1	CD33 MOUSE	Q63994 mus musculu
37	112.5	7.1	700	2	Q8TGO0	Q8TGO0 aspergillus
38	112.5	7.1	1795	2	Q6RJA3	Q76894 drosophila
39	112	7.0	233	2	Q6RJA3	Q6RJA3 homo sapien
40	111.5	7.0	369	2	Q46704	Q46704 fugu rubrip
41	111.5	7.0	506	1	SHS1_BOVIN	Q46631 bos taurus
42	111.5	7.0	509	1	SHS1_RAT	P97710 r protein-t
43	110	6.9	253	2	Q8UZE2	Q8UZE2 cercopithec
44	109.5	6.9	233	2	Q8N5F4	Q8N5F4 homo sapien
45	109.5	6.9	1225	2	Q6GPE1	Q6GPE1 xenopus lae

ALIGNMENTS

RESULT 1

ID	Q9UKJ1	PRELIMINARY;	PRT;	303 AA.
AC	Q9UKJ1;			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)			
DE	Inhibitory receptor PILRalpha.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Mammalia; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20127940; PubMed=10660620; DOI=10.1074/jbc.275.6.4467;			
RA	Moussieu D.D., Banville D., L'Abbe D., Bouchard P., Shen S.H.;			
RT	"PILRalpha, a novel immunoreceptor tyrosine-based inhibitory motif-			
RT	bearing protein, recruits SHP-1 upon tyrosine phosphorylation and is			
RT	paired with the truncated counterpart PILRBeta.";			
RL	J. Biol. Chem. 275:4467-4474(2000).			
DR	EMBL; AF161080; AAD52964.1; "			
DR	Gene; HGNC:20396; PILRA.			
DR	GO; GO:0005887; C:Integral to plasma membrane; ISS.			
DR	GO; GO:0005515; F:protein binding; ISS.			
DR	GO; GO:0007171; P:transmembrane receptor protein tyrosine kin. . .; ISS.			
DR	InterPro; IPR003599; IG.			
DR	InterPro; IPR007110; IG-like.			
DR	SMART; SM00409; IG; 1.			
DR	PROSITE; PS50835; IG_LIKE; 1.			
KW	Receptor.			
SC	SEQUENCE 303 AA; 33877 MW; 0410ADFC7E80928B CRC64;			
Query Match				
Best Local Similarity 99.8%; Score 1588; DB 2; Length 303;				
Matches 302; Conservative 1; Mismatches 0; Indels 0; Gaps 0;				
QY	1	MGRPLLPPLLPPLPPAPLQPSGSGPSLYGVTPQKHSAMGSGVEIPFSFYWE	60	
DB	1	MGRPLLPPLLPPLPPAPLQPSGSGPSLYGVTPQKHSAMGSGVEIPFSFYWE	60	
QY	61	LATPVDVIRSRGPHFGQSFYSTRPPIHNDYVNRFLNMTGOKSGFLRISNLOKODQ	120	
DB	61	LATPVDVIRSRGPHFGQSFYSTRPPIHNDYVNRFLNMTGOKSGFLRISNLOKODQ	120	
QY	121	SVYFCRVELDTRSSGRQOGSIEGSKLSITQAVTTTTPRPSMTTWRSLSTTTTGIRV	180	
DB	121	SVYFCRVELDTRSSGRQOGSIEGSKLSITQAVTTTTPRPSMTTWRSLSTTTTGIRV	180	
QY	181	TQGRSRDSWHISLETAVGVAVATVVGIMTLGILCLRWRRRGQORTKATPARBEPQ	240	
DB	181	TQGRSRDSWHISLETAVGVAVATVVGIMTLGILCLRWRRRGQORTKATPARBEPQ	240	
QY	241	NTEEPYENIRNEGQNTDPKLNPKDGLVYASIALSSSTSPAPSHPLKSPQNETLYSV	300	
DB	241	NTEEPYENIRNEGQNTDPKLNPKDGLVYASIALSSSTSPAPSHPLKSPQNETLYSV	300	

Db 241 NTEEPYENIRNEGQNTDPKLNPKDDGIYVASLALSSSTSPKAPPSPHRLKSPONETLYSV 300
 Qy 301 LKA 303
 Db 301 LKA 303

RESULT 2

08NH11 PRELIMINARY; PRT; 226 AA.
 AC 08NH11;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE PILRB protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.

RC TISSUE=Lung;
 RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Borkak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butcherfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RA Strauberg R.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL, BC017812; AAH17812.1; -.
 DR InterPro; IPR003599; IG, 1.
 DR InterPro; IPR007110; IG-like.
 DR SMART; SM00409; IG, 1.
 DR SMART; PSS0835; IG LIKE; 1.
 SQ SEQUENCE 226 AA; 25478 MW; 5938181797733A30 CRC64;

Query Match 62.7%; Score 997.5; DB 2; Length 226;
 Best Local Similarity 67.8%; Pred. No. 5,7e-75;
 Matches 196; Conservative 6; Mismatches 10; Indels 77; Gaps 2;

Qy 1 MGRPLLLPLPLLPALPFLQPSGSGTSGPSYLYGVTPQPKLSASMGSGVEIPPSFYYPWE 60
 Db 1 MGRPLLLPLPLLPALPFLQPSGSGTSGPSYLYGVTPQPKLSASMGSGVEIPPSFYYPWE 60
 Qy 61 LATAPDVRIISMRGRHFGHGFSGFYSTRPSIHKDYVNRFLFNMTEGQSGFLRISNLQKODQ 120
 Db 61 LATAPDVRIISMRGRHFGHGFSGFYSTRPSIHKDYVNRFLFNMTEGQSGFLRISNLQKODQ 120
 Qy 121 SVYFCRVELDTRSSGRQOMOSIEGTSLSTQAVTTTTPRPSMTTWRLSTTTTGLRV 180
 Db 121 SVYFCRVELDTRSSGRQOMOSIEGTSLSTQAVTTTTPRPSMTTWRLSTTTTGLRV 180
 Qy 181 TQGRKRSDSWHISLETAVGAAVAATVLTGIMLGLICLLRMRRRRGQRTAATPPAREPFQ 240
 Db 181 TQGRKRSDSWHISLETAVGAAVAATVLTGIMLGLICLLRMRRRRGQRTAATPPAREPFQ 240

Db 152 -----GOQRTAATPPAREPFQ 167
 Qy 241 NTEEPYENIRNEGQNTDPKLNPKDDGIYVASLALSSSTSPKAPPSPHRLK 289
 Db 168 NTEEPYENIRNEGQNTDPKLNPK-----LHUTOSTSQPSQPPERPDV 212

RESULT 3

09UKJ0 PRELIMINARY; PRT; 227 AA.
 AC 09UKJ0;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Activating receptor PILRBeta (Hypothetical protein DKFZp4340079).
 GN Name=DKFZp4340079;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.

RC TISSUE=Testis;
 RX MEDLINE=20127940; PubMed=10660620; DOI=10.1074/jbc.275.6.4467;
 RA Mousseau D.D., Banville D., L'Abbe D., Bouchard P., Shen S.H.,
 RT bearing protein, recruits SHP-1 upon tyrosine phosphorylation and is
 RT paired with the truncated counterpart PILRBeta.";
 RL J. Biol. Chem. 275:4467-4474(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RA The German cDNA Consortium;
 RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
 RA Mewes H.W., Weil B., Amdt C., Oeanger A., Fobbe G., Han M., Wiemann S.;
 RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF161081; AAD52965.1; -.
 DR EMBL; AL834336; CAH10711.1; -.
 DR Inctact; Q9UKJ0; -.
 DR GO; GO:0005887; C:integral to plasma membrane; NAS.
 DR GO; GO:0005515; F:protein binding; IPT.
 DR GO; GO:0007171; P:transmembrane receptor protein tyrosine kin. .; NAS.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR SMART; SM00409; IG, 1.
 DR SMART; PSS0835; IG LIKE; 1.
 KW Hypothetical protein; Receptor.
 SQ SEQUENCE 227 AA; 25542 MW; 7FF960C60AB7EF09 CRC64;

Query Match 60.2%; Score 958; DB 2; Length 227;
 Best Local Similarity 80.8%; Pred. No. 1.1e-71;
 Matches 185; Conservative 15; Mismatches 19; Indels 10; Gaps 2;

Qy 1 MGRPLLLPLPLLPALPFLQPSGSGTSGPSYLYGVTPQPKLSASMGSGVEIPPSFYYPWE 60
 Db 1 MGRPLLLPLPLLPALPFLQPSGSGTSGPSYLYGVTPQPKLSASMGSGVEIPPSFYYPWE 60
 Qy 61 LATAPDVRIISMRGRHFGHGFSGFYSTRPSIHKDYVNRFLFNMTEGQSGFLRISNLQKODQ 120
 Db 61 LATAPDVRIISMRGRHFGHGFSGFYSTRPSIHKDYVNRFLFNMTEGQSGFLRISNLQKODQ 120
 Qy 121 SVYFCRVELDTRSSGRQOMOSIEGTSLSTQAVTTTTPRPSMTTWRLSTTTTGLRV 180
 Db 121 SVYFCRVELDTRSSGRQOMOSIEGTSLSTQAVTTTTPRPSMTTWRLSTTTTGLRV 180
 Qy 181 TQGRKRSDSWHISLETAVGAAVAATVLTGIMLGLICLLRMRRRRGQRTAATPPAREPFQ 240
 Db 173 TBSKGSBSWHISLETAIRVALAVATVLTGIMLGLICLLRMRRRRGQRTAATPPAREPFQ 221
 RESULT 4
 Q8BYA6 PRELIMINARY; PRT; 299 AA.
 ID Q8BYA6
 AC Q8BYA6;

DT 01-MAR-2003 (Tremblé,rel. 23, Created)
DT 01-MAR-2003 (Tremblé,rel. 23, Last sequence update)
DT 01-OCT-2003 (Tremblé,rel. 23, Last annotation update)
DE Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched
DE library, clone:630007P20 product:weakly similar to INHIBITORY
DE RECEPTOR P1LALPHA.
GN Name=P1tra; Synonym=AV021745;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteleota; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
[1]
RN RP SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Thymus;
RC MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RX RA Carninci P., Hayashizaki Y.,
RT "High-efficiency full-length cDNA cloning";
RL Mech. Enzymol. 303:19-44(1999).
[2]
RN RP SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Thymus;
RC MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RX RA Carninci P., Hayashizaki Y.,
RT "High-efficiency full-length cDNA cloning";
RL Mech. Enzymol. 303:19-44(1999).
[3]
RN RP SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Thymus;
RC The FANTOM Consortium.
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RL Nature 420:563-573(2002).
[4]
RN RP SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Thymus;
RC MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RX RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RT Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
RL "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes".
RL Genome Res. 10:1617-1630(2000).
[5]
RN RP SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Thymus;
RC MEDLINE=20530913; PubMed=1076661; DOI=10.1101/gr.152600;
RX RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishii K., Kitesuna T., Tashiro H., Itoh M.,
RA Suni N., Ishii Y., Nakemura S., Hazama M., Nishino T., Harada A.,
RAYanamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kasahagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanishi M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[6]
RN RP SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Thymus;
RC Adechi J., Aizawa K., Akimura T., Arikawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Yanamoto K., Hirakawa T., Hirakawa T.,
RA Horii F., Imocani K., Ishii Y., Itoh M., Kagawa I., Kanakawa T.,
RA Kachi H., Kawai J., Kojima Y., Kondo S., Kono H., Konda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numasaki R., Ohno M., Ohnishi N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toyu T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
OR EMBL; AK041413; BAC30935.1; -.
OR MGD; MGI:2450529; P1tra.

Query Match	39.6%	Score 630;	DB 2;	Length 299;
Best Local Similarity	44.4%	Pred. NO.3.2e-44;		
Matches 136;	Conservative 56;	Mismatches 96;	Indels 18;	Gaps 6
DR	GO:0004872; F:receptor activity; IEA.			
DR	Interfero; IPR007110; Ig-like.			
KW	Receptor.			
DR	SEQUENCE 299 AA; 32992 MW; C1158DC3E1B3F74F CRC64;			
QY	5 LLLPLPLPLP-----PAFLQPSGSGTSGSPSYLVGYTQPKHLASMGSGVEIPFSFY 57			
DB	4 VVLSMFPTVTCSSGRVSPSF--PONSRSNRKNGFGVNOGESCGVGGSIDIPFSFYF 61			
QY	58 FWEIATADVARIWMRGHFHFGQSFYSTRPSPHKOYVNRFLNMTGQSGFLRISLQK 117			
DB	62 FWKLAKDQFQMSIAWRMKDFHGFHFNSSLPFIHEHFKRLILNMTQGSGLRLINKKE 121			
QY	118 QDQSVYFPRVLDLRRSSGRQOMQSIEGKLSITQAVTTTQRPSPMTTWLSSITTTTG 177			
DB	122 SDQRTFFRVLQQT--TSGIQFMQSTPGTQLNVTATCTPTLLPST-----TAATSHTQ 174			
QY	178 LRVTKGRSDSPWHISLETAVGVAVVVLIMIGLICLDRWRKQGRKATTPARE 237			
DB	175 NDITFVK-SANIGGLDLOTTYGATPAVLVGLVGLVFLPMKRRGQGTKEIPARE 233			
QY	238 PFQNTPEYENIRNEGQNTDPKLNPKDDGIYVASIALSSSTSPRAPSPHRLPKSPQNETL 297			
DB	234 PLE-TSEKHGSVGHGQCQMDKPKENDKDNNIYVASISLSSPTSPGTAFLPVHGNPQESTV 292			
QY	298 YSVLKA 303			
DB	293 YSIYCA 298			
RESULT 5				
AXL2_YEAST	STANDARD;	PRT;	823 AA.	
ID	AXL2_YEAST			
AC	P38928; Q96VY8;			
DT	01-FEB-1995 (Rel. 31, Created)			
DT	01-FEB-1995 (Rel. 31, Last announcement update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	AXL2 protein precursor (SRO4 protein).			
GN	Name=AXL2; Synonyms=REV7, SRO4; Order=diocusNames=YI1140W;			
OS	Saccharomyces cerevisiae (Baker's yeast).			
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;			
OC	Saccharomycetales; Saccharomycetaceae; Saccharomycetes.			
OX	NCBI_TextID=4932;			
RN	(1)			
RP	SEQUENCE FROM N.A.			
RA	Roemer T., Madden K., Chang J., Snyder M.;			
RL	Submitted (MAY-1996) to the EMBL/Genbank/DBJ databases.			
RP	(2)			
RC	SEQUENCE FROM N.A.			
RC	STRAIN=S288c / AB972;			
RX	MEDLINE=97313266; PubMed=9169870;			
RA	Church C.M., Bowman S., Badcock K., Bankier A., Brown D.,			
RA	Chillingworth T., Connor R., Devlin K., Gentles S., Hamlin N.,			
RA	Harris D.E., Horenell T., Hunt S., Jagels K., Jones M., Lye G.,			
RA	Moule S., Odell C., Pearson D., Rajadream M.A., Rice P., Rowley N.,			
RA	Skellton J., Smith V., Walsh S., Whitehead S., Barrett B.G.;			
RT	"The nucleotide sequence of Saccharomyces cerevisiae chromosome IX."			
RL	Nature 387:84-87(1997).			
RN	(3)			
RP	SEQUENCE OF 1-775 FROM N.A.			
RA	Matthew P.W.;			
RL	Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.			
RN	(4)			
RP	SEQUENCE OF 80-823 FROM N.A.			
RA	Torrey L.E., Gibbs P.E.M., Nelson J., Lawrence C.W.;			
RL	Submitted (MAR-1994) to the EMBL/Genbank/DBJ databases.			
RN	(5)			
RP	INTERACTION WITH BUD5.			
RX	PubMed=11313501; DOI=10.1126/science.1060360;			

RA Kang P.J., Sanson A., Lee B., Park H.-O.;
RT "A GNP/GMP exchange factor involved in linking a spatial landmark to
RT cell polarity".
RL Science 292:1376-1378(2001).
CC -|- FUNCTION: Required for axial budding pattern.
CC -|- SUBUNIT: Interacts with BUD5.
CC -|- SUBCELLULAR LOCATION: Must be delivered to the plasma membrane via
CC the secretory pathway. Once anchored in the plasma membrane, it
CC may recruit additional components to the incipient bud site.
CC -----
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CC -----
DR EMBL; U49845; AAA98666.1; -;
DR EMBL; Z38059; CAA86138.1; -;
DR EMBL; AF395906; AAK83884.1; -;
DR EMBL; U07228; AAA67919.1; -;
DR PIR; S48394; S48394.
DR GeneMOnline; 139675; -;
DR SGD; S000001402; AXL2.
DR InterPro; IPR006644; Ccdg.
DR InterPro; IPR008009; He_PIC.
DR Pfam; PF05345; He_PIC; I.
DR SMART; SM00736; CADG; 4.
KW Glycoprotein; Signal; Transmembrane.
FT SIGNAL 1 22 potential.
FT CHAIN 23 823 AXL2 protein.
FT TRANSMEM 509 529 potential.
FT CARBOHYD 41 41 N-linked (GlcNAc...) (potential).
FT CARBOHYD 50 50 N-linked (GlcNAc...) (potential).
FT CARBOHYD 96 96 N-linked (GlcNAc...) (potential).
FT CARBOHYD 117 117 N-linked (GlcNAc...) (potential).
FT CARBOHYD 163 163 N-linked (GlcNAc...) (potential).
FT CARBOHYD 260 260 N-linked (GlcNAc...) (potential).
FT CARBOHYD 266 266 N-linked (GlcNAc...) (potential).
FT CARBOHYD 304 304 N-linked (GlcNAc...) (potential).
FT CARBOHYD 324 324 N-linked (GlcNAc...) (potential).
FT CARBOHYD 359 359 N-linked (GlcNAc...) (potential).
FT CARBOHYD 382 382 N-linked (GlcNAc...) (potential).
FT CARBOHYD 389 389 N-linked (GlcNAc...) (potential).
FT CARBOHYD 403 403 N-linked (GlcNAc...) (potential).
FT CARBOHYD 447 447 N-linked (GlcNAc...) (potential).
FT CARBOHYD 451 451 N-linked (GlcNAc...) (potential).
FT CARBOHYD 495 495 N-linked (GlcNAc...) (potential).
FT CARBOHYD 595 595 N-linked (GlcNAc...) (potential).
FT CARBOHYD 649 649 N-linked (GlcNAc...) (potential).
FT CARBOHYD 663 663 N-linked (GlcNAc...) (potential).
FT CARBOHYD 737 737 N-linked (GlcNAc...) (potential).
FT CARBOHYD 803 803 N-linked (GlcNAc...) (potential).
SQ SEQUENCE 823 AA; 90783 MW; 350D79758BF30771 CRC64;
Query Match 9.1%; Score 144.5; DB 1; Length 823;
Best Local Similarity 24.7%; Pred. No. 0.0031;
Matches 72; Conservative 45; Mismatches 96; Indels 79; Gaps 16;

DB 476 ISTSAATSSA.PALPANKTSSHN---KKAVALACGVALPGLVLLALICFLIPWRR 532
QY 224 KGOQRK-----ATTPAREPQNTREYEYENIRNGCTDPRLANKXD 265
DB 533 RNPDOENLPHAIISGPDLLNPNANKPNQ-----ENATPLNPFDD 571
RESULT 6
ID 06UX24 PRELIMINARY; PRT; 290 AA.
AC 06UX24;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE PIGR.
GN Oryzomys=UNQ3105;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Haas P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seeshagiri S., Simons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vashden R., Watanabe C., Weand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan Y., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
DR EMBL; AY358545; AAQ88909.1; -;
DR InterPro; IPR001986; EPPS_synth.
DR InterPro; IPR003599; IG_1like.
DR InterPro; IPR007110; IG_1like.
DR SMART; SM00409; IG_1.
DR PROSITE; PS00104; EPPS_SYNTHASE_1; UNKNOWN_1.
DR PROSITE; PS50835; IG_Like; 1.
SQ SEQUENCE 290 AA; 32335 MW; B3D84A6B417AB941 CRC64;
Query Match 8.7%; Score 139; DB 2; Length 290;
Best Local Similarity 23.7%; Pred. No. 0.0024;
Matches 78; Conservative 49; Mismatches 126; Indels 76; Gaps 16;
QY 7 LPLPLPLLPAPFAGSGSTGSPSYLYGVTPKHLASMGSGVEIPFSFYPMELATAPD 66
DB 1 MPLTLTYLLPLF-----SGYSTATQITGTPYVNGLEKSLITQCVVRSGEYTLK-- 51
QY 67 VRIWRGPHFGOSFYSTRPPIHKDYVNRFLNLTGEGKSGFLRIS--NLQKODSVYF 124
DB 52 ---WMCRGAIWPDCKILVTSGSEGE-VKRDVSIKDNQKNTFTYVMDLMTADFTY 107
QY 125 CRVELDTRSSGQOQMSIGTGLSTQAVTTTQRPSSMTTWRSLSTTTTGLRVTQK 184
DB 108 CGIEK-----TGNDLGVTVQVITD--PAPVTOE-ETSSSPFLTG----- 143
QY 185 RSDSWHISLETAAGVAVAVTVYGLIILGLILKLRKRRKGOORTATTPAR--EPPQNT 242
DB 144 HHLDRHKLKLSVLLPLFTLL-LILLVAASLLMRMKYQQAAGSPFQVLOPLDG- 201
QY 243 EEPYENIRNEGQNTD-----KLN-----EKDDGIYVASIALSSSTSP 280
DB 202 DLCAVDLTQLAGTSRKAATTKLSSAQNQVQVEVEYVYTNASLPRED-ISAASLTIGA--ED 258
QY 281 RAB-----PSHRPLKSPQNETLYSVL 301
DB 259 QEPYCNMGLSHSLPGRGPPEPTXYSTI 287

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RESULT 7
Q726A6 PRELIMINARY; PRT; 290 AA.
ID Q726A6 AC
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Inhibitory receptor IREMI.
GN Name=IREMI;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RA Alvarez-Errico D., Kitzig F., Sayos J., Lopez-Botet M.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY303545; AAF57942.1; -.
DR HSSP: O95944; IHKF.
DR GO: GO:0004872; F:receptor activity; IEA.
DR InterPro: IPR001986; EBPSP_synth.
DR InterPro: IPR003599; IG.
DR InterPro: IPR007110; IG-like.
DR SMART: SM00409; IG; 1.
DR PROSITE: PS00104; EBPSP_SYNTHASE_1; UNKNOWN_1.
DR PROSITE: PS50835; IG_LIKE; 1.
DR RECEPTOR.
SQ SEQUENCE 290 AA; 32354 MW; E9D84A6B417AA9B CRC64;

Query Match 8.7%; Score 139; DB 2; Length 290;
Best local similarity 23.7%; Pred. No. 0.0024;
Matches 78; Conservative 49; Mismatches 126; Indels 76; Gaps 16;

QY 7 LPLPLLPAPLQPSGSGSYLYGVTPQPKHLSAMGSGVEIPFSFYYPWELATAPD 66
DB 1 MPLLTLYLLFWL-----SGYSIAIQITGPTVNGLERSLTVQCVYRSGMETYLK-- 51
QY 67 VRISWRGHFGQSFYSTRPSIHKDYVNRFLNMTGEGQSGFLRIS--NLQKODQSYVF 124
DB 52 ---WMCRAIWRDCKILVKTSGSQE--VKRDVSIKDNQKRTFTVTEMLMKTADATY 107
QY 125 CRVELDTRSSGRQMGOSIEGFKLSITQAVTTTQPPSSMTTWRLSSTTTTGLRVYQ 184
DB 108 CGIERK-----TGNDLGVTQVITD--PAPVTOE-ETSSSPITLTG----- 143
QY 185 RRSDSWHISLETAAGVAVAVVIGIMILGLICLRMRKQKQRTKATTPAR--EPQNT 242
DB 144 HHLNDRHKLKLSVLLPLIFTL--LLLVAAASLLAMRMKTYQQAAGMSPEQVLQPLEG- 201
QY 243 EEPYENIRNEGQNTDP-----KLN-----PKDDGIYASIALSSSTSP 280
DB 202 DLCAVDLTQLAGTSPPKATTKLSAQVDQVEVEYVTMAISLPKED--ISYASITLGA--ED 258
QY 281 RAP-----PSHRPLKSPQNETLYSVL 301
DB 259 QEPYCNMGHLSHLPGRGPPEPTEYSTI 287

RESULT 8
Q8TD01 PRELIMINARY; PRT; 290 AA.
ID Q8TD01 AC
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE NK inhibitory receptor.
GN Name=NKIR;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
```

```
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15184070; DOI=10.1016/j.jbirc.2004.05.065;
RA Sut L., Li N., Liu Q., Zhang W., Wan T., Wang B., Luo K., Sun H.,
RA Cao X.;
RT "IGSF1, a novel human inhibitory receptor of the immunoglobulin
RT superfamily, is preferentially expressed in dendritic cells and
RT monocytes.";
RL Biochem. Biophys. Res. Commun. 319:920-928(2004).
DR EMBL: AF251706; AAM19099.1; -.
DR HSSP: O95944; IHKF.
DR GO: GO:0004872; F:receptor activity; IEA.
DR InterPro: IPR001986; EBPSP_synth.
DR InterPro: IPR003599; IG.
DR InterPro: IPR007110; IG-like.
DR SMART: SM00409; IG; 1.
DR PROSITE: PS00104; EBPSP_SYNTHASE_1; UNKNOWN_1.
DR PROSITE: PS50835; IG_LIKE; 1.
DR RECEPTOR.
SQ SEQUENCE 290 AA; 32395 MW; D14FC04A047AAD10 CRC64;

Query Match 8.5%; Score 136; DB 2; Length 290;
Best local similarity 23.7%; Pred. No. 0.0042;
Matches 78; Conservative 48; Mismatches 127; Indels 76; Gaps 16;

QY 7 LPLPLLPAPLQPSGSGSYLYGVTPQPKHLSAMGSGVEIPFSFYYPWELATAPD 66
DB 1 MPLLTLYLLFWL-----SGYSIAIQITGPTVNGLERSLTVQCVYRSGMETYLK-- 51
QY 67 VRISWRGHFGQSFYSTRPSIHKDYVNRFLNMTGEGQSGFLRIS--NLQKODQSYVF 124
DB 52 ---WMCRAIWRDCKILVKTSGSQE--VKRDVSIKDNQKRTFTVTEMLMKTADATY 107
QY 125 CRVELDTRSSGRQMGOSIEGFKLSITQAVTTTQPPSSMTTWRLSSTTTTGLRVYQ 184
DB 108 CGIERK-----TGNDLGVTQVITD--PAPVTOE-ETSSSPITLTG----- 143
QY 185 RRSDSWHISLETAAGVAVAVVIGIMILGLICLRMRKQKQRTKATTPAR--EPQNT 242
DB 144 HHLNDRHKLKLSVLLPLIFTL--LLLVAAASLLAMRMKTYQQAAGMSPEQVLQPLEG- 201
QY 243 EEPYENIRNEGQNTDP-----KLN-----PKDDGIYASIALSSSTSP 280
DB 202 DLCAVDLTQLAGTSPPKATTKLSAQVDQVEVEYVTMAISLPKED--ISYASITLGA--ED 258
QY 281 RAP-----PSHRPLKSPQNETLYSVL 301
DB 259 QEPYCNMGHLSHLPGRGPPEPTEYSTI 287

RESULT 9
Q72715 PRELIMINARY; PRT; 293 AA.
ID Q72715 AC
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Immune receptor expressed on myeloid cells splice variant 1.
GN Name=IREMI;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RA Alvarez-Errico D., Kitzig F., Sayos J., Lopez-Botet M.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF375480; AAF42152.1; -.
DR HSSP: O95944; IHKF.
DR GO: GO:0004872; F:receptor activity; IEA.
DR InterPro: IPR003599; IG.
DR InterPro: IPR007110; IG-like.
DR SMART: SM00409; IG; 1.
```

DR	PROSITE; PS50835; IG_LIKE; 1.
KM	Receptor.
SO	SEQUENCE 293 AA; 32655 MW; 66EBEA2F8D3CF43E CRC64;
	Query Match 8.5%; Score 135.5; DB 2; Length 293;
	Best Local Similarity 22.8%; Pred. No. 0.0047;
	Matches 75; Conservative 51; Mismatches 128; Indels 75; Gaps 16
OY	7 LPLPLPLIPPAFLQPSGSGSPSYLYGVTPQKHLASMGSGVEIPFSFYYPWELATAPD 66
DB	3 LPLQDL-----MRVISAQSGSYSTATQITGPTTVNGLERGLATVQCVRSGMFTYLK-- 54
OY	67 VRISMRGHFHGQSGSYSTRPESIHKDVNRLPLMNTBQKSGFLAIS--NLQKQGSYVF 124
DB	55 --WRCRAIMRDKCKILVKTSGSEB--VKRDVRSIKDKQKNTFTVMEDLMKTDADTYW 110
OY	125 CRVELDTRSSGRQMGSIETGYLSITQAVTTTQTPSPSSMTTWRSLSTTTTGLRLVQK 184
DB	111 CGIER-----TGNDLSTGVQYTIID--PAPVQGE-ELSSSPILTG----- 146
OY	185 RRSDSWHSISLETAVGVAVAVTYLGIMILGLICLLMRRRKQQRKATKATTPAR--EPQNT 242
DB	147 HHLDRHRLKTLKLSVLLPLIFLTL-LLLVASLAWRMWKYQQAAGMSPEQVQLPLSG- 204
OY	243 EEPYENINNEGQNDTP-----KLN-----PKDGIYIASIALSSSTSP 280
DB	205 DLCAVDLLTQQAQGSIPRAKATTKLSAQQVDQVEVEYVTWASLPKED-ISVASLTIGA--ED 261
OY	281 RAP-----PSHRPLKSPONETLYSVL 301
DB	262 QEPYCNMGHLSHLPGRGPEPTTYSTI 290
RESULT 10	
SILE_HUMAN	
ID	SILE_HUMAN STANDARD; PRT; 499 AA.
AC	Q9NYZ4;
DT	28-FEB-2003 (Rel. 41, Created)
DT	28-FEB-2003 (Rel. 41, Last sequence update)
DT	25-OCT-2004 (Rel. 45, Last annotation update)
DE	Sialic acid binding Ig-1-like lectin 8 precursor (Siglec-8)
DE	(Sialoadhesin family member-2) (SAF-2).
GN	Name=SIGLEC8; Synonyms=SAF2;
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Euteria; Primates; Carnivora; Hominoidea; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A. (ISOFORM 1).
RX	MEDLINE=20549027; PubMed=11095983; DOI=10.1006/birc.2000.3866;
RA	Fousias G., Yousef G.M., Diamandis E.P.;
RA	"Molecular characterization of a siglec8 variant containing
RT	cytoplasmic tyrosine-based motifs, and mapping of the siglec8 gene.";
RL	Biochem. Biophys. Res. Commun. 278:775-781(2000).
RN	[2]
RP	SEQUENCE FROM N.A. (ISOFORM 3).
RX	MEDLINE=20315554; PubMed=1085641; DOI=10.1067/mai.2000.107127;
RA	Kidley K.K., Bochner B.S., Freeman S.D., Tan K.B., Gallagher K.T.;
RA	P'Allesio K.J., Holmes S.D., Abrahamson J.A., Erickson-Miller C.L.;
RA	Murdock P.R., Tachimoto H., Schleimer R.P., White J.R.;
RT	"Identification of SAF-2, a novel siglec expressed on eosinophils,
RT	mast cells, and basophils.";
RL	J. Allergy Clin. Immunol. 105:1093-1100(2000).
RN	[3]
RP	SEQUENCE FROM N.A. (ISOFORM 3).
RC	TISSUE=Eosinophil;
RX	MEDLINE=20092847; PubMed=10625619; DOI=10.1074/jbc.275.2.861;
RA	Floyd H., Ni Y., Cornish A.L., Zeng Z., Liu D., Carter K.C., Steel J.;
RA	Crocker P.R.;
RT	"Siglec-8, A novel eosinophil-specific member of the immunoglobulin
RT	superfamily.";
RL	J. Biol. Chem. 275:861-866(2000).
RN	[4]

RP	SEQUENCE FROM N.A. (ISOFORM 2).	
RA	Playa H., Zhang J.Q., Crocker P.R.;	
RL	Submitted (Oct-2000) to the EMBL/GenBank/DBJ databases.	
CC	-1- FUNCTION: Putative adhesion molecule that mediates static acid dependent binding to cells. Preferentially binds to alpha2,3-linked static acid. Also binds to alpha2,6-linked static acid. The static acid recognition site may be masked by cis interactions with static acids on the same cell surface.	
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.	
CC	-1- ALTERNATIVE PRODUCTS:	
CC	Event=Alternative splicing; Named isoforms=3;	
CC	Name=1; Synonyms=Long;	
CC	IsoId=Q9NTY4-1; Sequence=Displayed;	
CC	Name=2;	
CC	IsoId=Q9NTY4-2; Sequence=VSP_002559;	
CC	Name=3;	
CC	IsoId=Q9NTY4-3; Sequence=VSP_002560;	
CC	-1- TISSUE SPECIFICITY: Expressed specifically on eosinophils.	
CC	-1- DOMAIN: Contains 1 copy of a cytoplasmic motif that is referred to as the immunoreceptor tyrosine-based inhibitor motif (ITIM). This motif is involved in modulation of cellular responses. The phosphorylated ITIM motif can bind the SH2 domain of several SH2-containing phosphatases.	
CC	-1- SIMILARITY: Belongs to the immunoglobulin superfamily. SIGLEC (static acid binding Ig-like lectin) family.	
CC	-1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.	
CC	-1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.	
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CC	-----	
DR	EMBL, AF287892; AAC0573.1; -	
DR	EMBL, AF223403; AAF34702.1; -	
DR	EMBL, AF195093; AAF27622.1; -	
DR	EMBL, AF310234; AAK55140.1; -	
DR	HSSP; Q9Y286; 1075.	
DR	Genew: HGNC:10877; SIGLEC8.	
DR	MIM; 605639; -	
DR	GO; GO:0016021; C:integral to membrane; TAS.	
DR	GO; GO:0005529; F:sugar binding; TAS.	
DR	GO; GO:0005488; F:transmembrane receptor activity; TAS.	
DR	GO; GO:0007165; P:signal transduction; TAS.	
DR	InterPro; IPR007110; Ig-like.	
DR	InterPro; IPR003598; Ig_c2.	
DR	Pfam; PF00047; Ig; 2.	
DR	SMART; SM00408; IgC2; 1.	
KW	PROSITE; PS50835; IG LIKE; 2.	
KW	Alternative splicing; Cell adhesion; Glycoprotein; Immunoglobulin domain; Lectin; Repeat; Signal; Transmembrane.	
KW	SIGNAL	
FT	1	Potential.
FT	17	499
FT	17	363
FT	DOMAIN	364 384
FT	TRANSMM	385 499
FT	DOMAIN	40 123
FT	DOMAIN	157 240
FT	DOMAIN	246 344
FT	SITE	445 450
FT	SITE	468 473
FT	DISULFD	42 181
FT	DISULFD	47 107
FT	DISULFD	175 224
FT	DISULFD	283 328
FT	CARBOHYD	172 172
FT	CARBOHYD	249 249
FT	CARBOHYD	267 267
FT	VARSPLIC	152 245
FT	CAVSPDPTAARSVLTLPKPDHGSITLCQVTLPEPTGV	

Qy	65	PDVRI5MRGHHFGQSFYSTRPSP5IHKDYVRLFLNTEGQSGFL-----R1	112
Db	40	-----TCWYDLSLHNSDEKIMWC-----QIDNLCYLFVS-KSAEKPRFLIOOSSRFNFFVTM	90
Qy	113	SNLKQDQSGVYPCFQVRLDTRSSGRQMGQMSIEGTYKLSIQAVLTQTPRSSMTTWRLST	172
Db	91	TKLMSDGSIGHCGIAVNTNR-----IYIKRSIHLVYSKAS-TTWRTTTL	135
Qy	173	TTTTGRLVTOGKRKSDSMHISLEFVAVVAATVIGIMLGLICLRWRKRGQORTKAT	233
Db	136	ASHSSEVTNRSPDSDPMWK---AIVAGVVAVATLLTFVILLVYLKRAKRAKALNVQNC	192
Qy	233	TPAREPQNTPEEYENINRNGQNTDPKLNPKDDG-IYVASL-----ALSSSTSPR	288
Db	193	HPFYEDFSFOQKEETTSFNQOTHSSE-----DTGYCIYASLIHLNRVNPQDSIVSNTQPY	246
Qy	282	APPSHRPL 289	
Db	247	PKPSDPL 254	
RESULT 12			
Q8TBG9			
ID	Q8TBG9	PRELIMINARY;	PRT; 233 AA.
AC	Q8TBG9;		
DT	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)		
DE	Hypothetical protein.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Primary B-Cells;		
RC	MEBLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;		
RA	Strasbourg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuller G.D.,		
RA	Altschul S.F., Zeeberg B., Buercow K.H., Schaefer C.F., Bhat N.K.,		
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,		
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,		
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,		
RA	Brownstein M.J., Ushin T.B., Toshiyuki S., Carninci P., Prange C.,		
RA	Raba S.S., Longellano N.A., Peters G.J., Abramson R.D., Muliyil S.J.,		
RA	Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,		
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA	Faley J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,		
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		
RA	Blakeley R.C., Greenwood J., Schmutz J., Myers R.M., Butterfield Y.S.,		
RA	Krzywniak M.I., Skalska U., Smalius D.E., Scherch A., Schein J.E.,		
RA	Jones S.J., Marra M.A.;		
RT	"Generation and initial analysis of more than 15,000 full-length human		
RT	and mouse cDNA sequences.";		
RT	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Primary B-Cells;		
RA	Strasbourg R.;		
RL	Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; BC022823; AAH22823.1; -		
DR	PIR; S12442; S12442.		
DR	PIR; S30525; S30525.		
DR	PIR; S30526; S30526.		
DR	HSSP; P01842; 1LIL.		
DR	InterPro; IPR007110; Ig-like.		
DR	InterPro; IPR003597; Ig cl.		
DR	InterPro; IPR003006; Ig_MHC.		
DR	InterPro; IPR003596; Ig_V.		
DR	Pfam; PF07654; C1-sec; 1.		

DR SMART; SMO0406; IGV: 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR Hypothetical protein.
SQ Hypothetical protein.
KW SEQUENCE 233 AA; 24867 MW; 367411BFD6F4DF92 CRC64;

Query Match 8.1%; Score 129.5; DB 2; Length 233;
Best Local Similarity 24.2%; Pred. NO. 0.011;
Matches 54; Conservative 32; Mismatches 64; Indels 73; Gaps 10.

OY 4 P L L L P L L P L P A F L O P S G S T G S P S Y L Y G V T O P K H L S A S M G S V E I -----PFS 54
D b 5 P L L P L I L T L -----C T G S E A S --Y E L T Q P S V S P S G C A R I T C S G D A L P K O Y A 51
OY 55 F Y P P E L A T A D V R I S M R G R H F H G S F P S T P S P S H K D Y N R L F L M W E G K S G ---FLR 111
D b 52 Y W Y O O K P E Q A P -V L V I Y I D -----N E R S G I P E P F -----S G S S S G T T V T L T 92
OY 112 I S N L Q K O D S Y V F C R V E L D P T R S S G R Q M S I E G T X L S I -----T Q A V T T T T O R P S S -----162
D b 93 I S G V Q A B E A D A Y Y Q C ----S A D S S G T Y V F P G G T K L T V L G G P K A P S T L L P P S S E L Q A 148

OY 163 -----M T T Y R L S T T T T T G L R V T Q G K R S D S 189
D b 149 N K A T L V C L I S D F P G A V T W A K K A D S P V K A G E V T T P S K O S N 191

RESULT 13
Q72728 PRELIMINARY; PRT; 499 AA.
ID Q72728
AC Q72728;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Hypoetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
KA Kleusner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.B., Rubin G.M., Hong L.,
RA Stepien M., Soares M.B., Bonaldi M.P., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Uebin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Halys S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Hellon E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Buterfield Y.S.,
RA Krzywicki M.I., Skalski U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marx M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
LN [2]
RE SEQUENCE FROM N.A.
RP TISSUE=Spleen;
RC Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC053319; AAHS3319.1;
DR InterPro; IPRO07110; IG_1like.
DR InterPro; IPRO03598; IG_cg2.
DR Pfam; PF00047; Ig_2.
DR SMART; SMO0408; IGC2; 1.
DR

Query Match	Best Local Similarity	Matches	Score	DB 2	Length	DB 1
Query Match	Best Local Similarity	Matches	8.1%, Score 129.5;	DB 2	Length 499;	DB 1
22.6%, Pred. No. 0.029;	45; Mismatches 138;	Indels 101; Gaps 14;				
PROSITE: PS50835; IG_LIKE; 2.						
DR Hypothetical protein.						
5Q SEQUENCE 499 AA; 54052 MW; CA32EEF7A89A7D3D CRC64;						
5 LLLPLPLPLPPALQPSGSGTSGSPSYLYGTQPKHLSASMGSYELPFPSYPMELATA 64						
3 LLLLLPLPLMTGKQME--GDRQYDGDYLLQOE--LTVVQEGLCVHPGCSFSYPDDGWTD 58						
65 PD-VRISSRRGHFPGQSFYSTRPPIHNDYVRLFLMTGEG-----KSGFLRISN 114						
59 SDPHNGWYFRA---GDRFYQAPAPATNPP--DREVQAEIQGRFQLGDIMGNDGSLARD 113						
115 LQKDDQSYVFCRVF-----LDRSSGRQD-- 138						
114 ARKDDKSGYFRLRLBERGSMKMSYKQLNYYKTQLSVFVYALTRRPDILLGLTIESGHPNRL 173						
139 -----MOSIECTKLSIT-----QAVTTTQORPSMTTWMRLSFTTTTGL 178						
174 TCSVPWACKQSTPPMISITIGASVSSPGFTTARSSVLITLPKQDHGSLTQCVLPTGTGV 233						
179 RVTQGRKRSDS---WHISL-----ETAVGVAVAATVYLGIMILGICL-----L 218						
234 TTTSTVRLDVSYPNNLITMTVFQGDATPASTALGNGSSLSVLEGSLRLVCVANSNPAPRL 293						
219 RWRRRKGGQQRKATTPAPAREPQN--TEEPYENIRREGQNTDPKLPKXDGITYASIALSSS 277						
294 SWTR-----GSLTLCPSKSSNPGLLEPRVAVHRDEGEFTCRANQAQSGQHSLSLSIQNE 348						
278 TSPRAPP 284						
349 GTGTSRP 355						
RESULT 14						
06ZMC9 PRELIMINARY; PRT; 328 AA.						
06ZMC9						
06ZMC9; 06ZMC9;						
05-JUL-2004 (TREMBLrel. 27, Created)						
05-JUL-2004 (TREMBLrel. 27, Last sequence update)						
05-JUL-2004 (TREMBLrel. 27, Last annotation update)						
Hypothetical protein FLJ23996.						
Homo sapiens (Human).						
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.						
NCBI_TaxID=9606;						
11						
SEQUENCE FROM N.A.						
Kawabata A., Hikiiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,						
Okitani R., Ota T., Suzuki Y., Ohashi M., Nishi T., Shibahara T.,						
Tanaka T., Nakamura Y., Isegai T., Sugano S.;						
Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.						
EMBL; AK172835; BADI6800.1; .						
InterPro; IPR003599; IG-like.						
InterPro; IPR007110; IG-like.						
SMART; SM00409; IG; 1.						
PROSITE; PS50835; IG_LIKE; 1.						
SEQUENCE 328 AA; 35652 MW; 534D6D2E7F04C6B CRC64;						
Query Match	7.8%, Score 123.5; DB 2; Length 328;					
Best Local Similarity	20.3%, Pred. No. 0.054;					
Matches	72; Conservative 42; Mismatches 123; Indels 117; Gaps 15;					
12 LLLPPAFLOPSGS-----TSGGSPSYLYGVTPQKHLASMGSGSYELPFPSF 55						
7 LLACLANVLPLGSGVVRKIDITTEHLNMTYHSSPAQMSMGVPPREVAEADDAVLPCTF 66						
56 YYPWELATAPDVRISSRRGH-FHGSQSFYSTRP-----SIKQDVNRLFLNMTG 104						
67 THPRHVDGPELTAL-WPAGBPYAPQVPRCAARGSSEICPTALSHGRF--RLGPNPRN 123						

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OM protein - protein search, using sw model

Run on: June 1, 2005, 21:56:35 ; Search time 162 Seconds
(without alignments)
723.385 Million cell updates/sec

Title: US-10-777-524-2

Perfect score: 1591

Sequence: 1 MGRPLRLPLRLPLPAFLQ.....PSHRPLKSPQNETLYSVLKA 303

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Listing first 45 summaries

Database : A.GeneSeq.16Dec04:*

1: GeneSeq1980s:*

2: GeneSeq1990s:*

3: GeneSeq2000s:*

4: GeneSeq2001s:*

5: GeneSeq2002s:*

6: GeneSeq2003as:*

7: GeneSeq2003bs:*

8: GeneSeq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1591	100.0	303	2	AAW62772 Human Imm
2	1591	100.0	303	3	AAW62772 Human Imm
3	1588	99.8	303	8	ADP25129 PRO polyp
4	1176.5	73.9	230	3	AAW62772 Human Imm
5	1171.5	73.6	230	7	ADP25129 PRO polyp
6	1010.5	63.5	206	7	ADP25129 PRO polyp
7	973.5	61.2	226	2	AAW62772 Human Imm
8	973.5	61.2	226	2	AAW62772 Human Imm
9	967.5	60.8	226	2	AAW62772 Human Imm
10	967.5	60.8	226	2	AAW62772 Human Imm
11	958	60.2	227	3	AAW62772 Human Imm
12	958	60.2	227	3	AAW62772 Human Imm
13	958	60.2	227	3	AAW62772 Human Imm
14	958	60.2	227	3	AAW62772 Human Imm
15	945	59.4	227	3	AAW62772 Human Imm
16	934	58.7	238	6	ABG95537 Human sec
17	934	58.7	238	6	ABG95537 Human sec
18	934	58.7	238	6	ABG95537 Human sec
19	934	58.7	238	6	ABG95537 Human sec
20	927.5	58.3	228	8	ADH74202 Human sec
21	821	51.6	175	3	AAW62772 Human Imm
22	808	50.8	1012	4	ABG16869 Novel hum
23	808	50.8	1012	4	ABG16869 Novel hum
24	808	50.8	1012	4	ABG16869 Novel hum
25	808	50.8	1012	4	ABG16869 Novel hum

26	517	32.5	101	2	AAW75053 Fragment
27	517	32.5	101	5	ABG95514 Human nov
28	517	32.5	101	6	ABG95514 Human nov
29	517	32.5	101	7	ADH74471 Human sec
30	511	32.5	101	8	ADH74471 Human sec
31	411	25.8	224	5	ADH74471 Human sec
32	405.5	25.5	212	7	ADH74471 Human sec
33	222	14.0	99	2	AAW62773 Partial m
34	148.5	9.3	305	4	AAU14284 Human nov
35	146.5	9.2	305	4	AAU14284 Human nov
36	146.5	9.2	305	4	AAU14284 Human nov
37	146.5	9.2	305	5	AAU14284 Human nov
38	146.5	9.2	305	5	AAU14284 Human nov
39	146.5	9.2	305	8	ADH11832 Human the
40	146.5	9.2	305	8	ADH11832 Human the
41	146.5	9.2	305	8	ADH11832 Human the
42	146.5	9.2	305	8	ADH11832 Human the
43	145.5	9.1	305	8	ADH11832 Human the
44	139	8.7	290	4	AAW62772 Human mem
45	139	8.7	290	5	AAU83611 Human PRO

ALIGNMENTS

RESULT 1	AAW62772	standard; protein, 303 AA.
ID	AAW62772	
XX	AAW62772	
AC	AAW62772	
XX	AAW62772	
DT	23-SEP-1998	(first entry)
XX	Human immunoglobulin receptor designated FDF03.	
DE	Human immunoglobulin receptor designated FDF03.	
XX	Human, type I transmembrane protein; immunoglobulin-like domain; FDF03; activated monocyte; YB01; KTB03; control; development; differentiation; mammalian immune system; treatment; cancerous condition; degenerative condition; autoimmune response; transplantation rejection; graft versus host disease; inflammatory condition; diagnosis; drug screening.	
XX	Homo sapiens.	
OS	Homo sapiens.	
XX	WO9824906-A2.	
XX	11-JUN-1998.	
PD	11-JUN-1998.	
XX	05-DEC-1997;	97WO-US021101.
PF	06-DEC-1996;	96US-0032252P.
XX	09-DEC-1996;	96US-00762187.
PR	16-DEC-1996;	96US-0033181P.
PR	21-MAR-1997;	97US-0041279P.
XX	(SCHE) SCHERING CORP.	
PA	Adema GJ, Meynard L, Gorman DM, McClanahan TK, Zurawski SM; Zurawski G, Lanier IL, Phillips JH; WPI; 1998-333325/29.	
XX	N-PSDB; AAV38987.	
DR	New isolated activated monocyte cell gene(s) - used to develop products for treating e.g. cancer, degenerative conditions, autoimmune responses, transplant rejection or inflammatory conditions.	
PT	Claim 1; Page 60-61; 104pp; English.	
XX	The present sequence represents a human protein, FDF03, which is a type I transmembrane protein comprising an extracellular portion characterized by immunoglobulin-like domains, indicating that the protein is a receptor member of the immunoglobulin superfamily. The FDF03 gene is found in	

CC activated monocytes. The specification also describes other proteins
CC encoded by activated monocytes, which are designated YEO1 and KTS03. The
CC genes function in controlling development, differentiation, and/or
CC physiology of the mammalian immune system. The products can be used for
CC treating abnormal proliferation, regeneration, degeneration or atrophy.
CC They can be used for treating e.g. cancerous conditions, degenerative
CC conditions, autoimmune responses, transplantation rejection, graft versus
CC host disease, or inflammatory conditions. The products can also be used
CC for detection, diagnosis and drug screening

XX Sequence 303 AA;

Query Match 100.0%; Score 1591; DB 2; Length 303;
Best Local Similarity 100.0%; Pred. No. 6.7e-122;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGRPLLPPLPLPPLPAPFLQPSGSGSPSYLYGVTPQKLSASMGSGVEIPPSFYYPWE 60

Qb 1 MGRPLLPPLPLPPLPAPFLQPSGSGSPSYLYGVTPQKLSASMGSGVEIPPSFYYPWE 60

QY 61 LATAPDVRIISMRGHEFGHGSFYSTRPPIHKDYVNRFLFWTEGOKSGFLRISNLQKODQ 120

Db 61 LATAPDVRIISMRGHEFGHGSFYSTRPPIHKDYVNRFLFWTEGOKSGFLRISNLQKODQ 120

QY 121 SYVFCRVELDTRSSGRQOQSIIEGTLSTQAVTTTQRPSSMTTWRLSSTTTTGLRV 180

Db 121 SYVFCRVELDTRSSGRQOQSIIEGTLSTQAVTTTQRPSSMTTWRLSSTTTTGLRV 180

QY 181 TOGKRSDSWHISLETAAGVAVAVTVLGIMILGLICLLMRRRKGGQRTKATTPAREPFO 240

Db 181 TOGKRSDSWHISLETAAGVAVAVTVLGIMILGLICLLMRRRKGGQRTKATTPAREPFO 240

QY 241 NTEBPYENIRNEGONTDPKLNPKODGIVYASIALSSSTSPRAPSPHRLKSPONETLYSV 300

Db 241 NTEBPYENIRNEGONTDPKLNPKODGIVYASIALSSSTSPRAPSPHRLKSPONETLYSV 300

QY 301 LKA 303

Db 301 LKA 303

RESULT 2

AAB07443 ID AAB07443 standard; protein; 303 AA.

XX AAB07443;

XX 20-OCT-2000 (first entry)

DE A human monocyte-derived protein FDP03.

XX Human, monocyte-derived protein; FDP03; FDP03deltaTM, FDP03-S1;

KM FDP03-M14; FDP03-S2; haematopoietic cell; monocyte hyperplasia;

KM tissue rejection; inflammation; infection.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..19

FT Protein /note= "signal peptide"

FT Protein 20..303

XX /note= "mature protein"

XX MO200040721-A1.

XX 13-JUL-2000.

XX 29-DEC-1999; 99MO-US030004.

XX 31-DEC-1998; 98US-00223919.

XX 31-DEC-1998; 98US-00224604.

XX (SCHE) SCHERING CORP.

XX Bates E, Fournier N, Chaulus L, Garrone P;
XX WPI, 2000-465984/40.
XX N-PSDB; AAA58814.
XX Novel monocyte-derived polypeptides and polynucleotides, used to diagnose
XX diseases associated with changes in monocyte numbers, e.g. bacterial or
XX viral infections.

PS Claim 1; Page 32-33; 45pp; English.

XX The present sequence represents a human monocyte-derived protein. The
XX specification describes monocyte-derived proteins FDP03, FDP03deltaTM,
XX FDP03-S1, FDP03-M14, and FDP03-S2. The proteins are involved in the
XX regulation, or development, of haematopoietic cells. Antibodies specific
XX for antigenic components of the proteins can be used to detect the
XX components in samples. The proteins can also be used to screen for
XX candidate therapeutic agents. The monocyte-derived proteins and
XX polynucleotides can be used for diagnosis of diseases related to an
XX increase, or decrease, in the number of monocytes in a tissue or lymph
XX system, such as monocyte hyperplasia, tissue or graft rejection,
XX inflammation, or bacterial or viral infections. The proteins can also be
XX used in the treatment of disorders associated with abnormal expression or
XX signalling by a monocyte

XX Sequence 303 AA;

Query Match 100.0%; Score 1591; DB 3; Length 303;
Best Local Similarity 100.0%; Pred. No. 6.7e-122;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGRPLLPPLPLPPLPAPFLQPSGSGSPSYLYGVTPQKLSASMGSGVEIPPSFYYPWE 60

Db 1 MGRPLLPPLPLPPLPAPFLQPSGSGSPSYLYGVTPQKLSASMGSGVEIPPSFYYPWE 60

QY 61 LATAPDVRIISMRGHEFGHGSFYSTRPPIHKDYVNRFLFWTEGOKSGFLRISNLQKODQ 120

Db 61 LATAPDVRIISMRGHEFGHGSFYSTRPPIHKDYVNRFLFWTEGOKSGFLRISNLQKODQ 120

QY 121 SYVFCRVELDTRSSGRQOQSIIEGTLSTQAVTTTQRPSSMTTWRLSSTTTTGLRV 180

Db 121 SYVFCRVELDTRSSGRQOQSIIEGTLSTQAVTTTQRPSSMTTWRLSSTTTTGLRV 180

QY 181 TOGKRSDSWHISLETAAGVAVAVTVLGIMILGLICLLMRRRKGGQRTKATTPAREPFO 240

Db 181 TOGKRSDSWHISLETAAGVAVAVTVLGIMILGLICLLMRRRKGGQRTKATTPAREPFO 240

QY 241 NTEBPYENIRNEGONTDPKLNPKODGIVYASIALSSSTSPRAPSPHRLKSPONETLYSV 300

Db 241 NTEBPYENIRNEGONTDPKLNPKODGIVYASIALSSSTSPRAPSPHRLKSPONETLYSV 300

QY 301 LKA 303

Db 301 LKA 303

RESULT 3

ADP25129 ID ADP25129 standard; protein; 303 AA.

XX ADP25129;

XX 18-NOV-2004 (first entry)

XX PRO polypeptide SEQ ID NO:2307.

XX PRO; antiinflammatory; antiatheritic; antirheumatic; immunosuppressive;

KM osteopathic; antidiabetic; dermatological; antiparasitic; antiallergic;

XX antisthmatic; hepatotropic; respiratory; gene therapy; immune system.

XX Unidentified.

PN WO2004041170-A2.
 XX 21-MAY-2004.
 PD
 XX 30-OCT-2003; 2003WO-US034312.
 XX
 XX 01-NOV-2002; 2002US-0423394P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 XX Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;
 P1 Wu TD;
 XX
 XX WPI: 2004-419628/39.
 DR N-PSDB; ADP25128.
 XX
 XX New PRO polypeptides and polynucleotides, useful for treating e.g.
 PT erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated
 PT renal disease, or demyelinating diseases of the central or peripheral
 PT nervous system.
 XX
 XX Claim 7; SEQ ID NO 2307; 2940bp; English.
 XX
 CC The invention relates to a novel isolated nucleic acid and the PRO
 CC polypeptide encoded by it. A protein of the invention has
 CC antiinflammatory, antirheumatic, antirheumatic, immunosuppressive,
 CC osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,
 CC antineoplastic, hepatocytic, and respiratory activity. A polynucleotide
 CC of the invention may have a use in gene therapy. The PRO polypeptide, its
 CC agonist, antagonist, or antibody that specifically binds to the
 CC polypeptide is useful for treating an immune related disorder such as
 CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
 CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
 CC idiopathic inflammatory myopathy, Sjogren's syndrome, autoimmune
 CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
 CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
 CC disease, a demyelinating disease of the central or peripheral nervous
 CC system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
 CC a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
 CC disease, infectious or autoimmune chronic active hepatitis, primary
 CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
 CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
 CC disease, an autoimmune or immune-mediated skin disease, a bullous skin
 CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
 CC disease, asthma, allergic rhinitis, atopic dermatitis, food
 CC hypersensitivity, urticaria, an immunologic disease of the lung,
 CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
 CC pneumonitis, a transplant-associated disease, graft rejection or
 CC graft-versus-host disease. The present sequence represents a PRO protein
 CC of the invention.
 XX
 XX Sequence 303 AA;
 SQ
 Query Match 99.8%; Score 1588; DB 8; Length 303;
 Best Local Similarity 99.7%; Pred. No. 1,2e-121;
 Matches 302; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 241 NTEPEYENIRNEGONTDPKLNPKDDGIYVYASLALSSSTSPRAPPSPHRLPKSPONETLYSV 300
 DB 241 NTEPEYENIRNEGONTDPKLNPKDDGIYVYASLALSSSTSPRAPPSPHRLPKSPONETLYSV 300
 OY 301 LKA 303
 DB 301 LKA 303
 RESULT 4
 AAB07444
 ID AAB07444 standard; protein; 230 AA.
 XX
 XX AAB07444;
 XX
 XX 20-OCT-2000 (first entry)
 XX
 DE A human monocyte-derived protein FDF03DeltaTM.
 XX
 XX Human; monocyte-derived protein; FDF03; FDF03DeltaTM; FDF03-S1;
 KW FDF03-M14; FDF03-S2; haematopoietic cell; monocyte hyperplasia;
 KW tissue rejection; inflammation; infection.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..17
 FT Protein /note= "signal peptide"
 FT Protein 18..230
 FT Protein /note= "mature protein"
 XX
 PN WO2004040721-A1.
 XX
 XX 13-JUL-2000.
 PD
 XX 29-DEC-1999; 99WO-US030004.
 PF
 XX 31-DEC-1998; 98US-00223919.
 PR 31-DEC-1998; 98US-00224604.
 XX
 PA (SCHE) SCHERING CORP.
 XX
 PI Bates E, Fournier N, Chalus L, Garrone P;
 XX
 DR WPI: 2000-465984/40.
 DR N-PSDB; AAB58815.
 XX
 PT Novel monocyte-derived polypeptides and polynucleotides, used to diagnose
 PT diseases associated with changes in monocyte numbers, e.g. bacterial or
 PT viral infections.
 XX
 XX Claim 1; Page 34-35; 45pp; English.
 XX
 CC The present sequence represents a human monocyte-derived protein. The
 CC specification describes monocyte-derived proteins FDF03, FDF03DeltaTM,
 CC FDF03-S1, FDF03-M14, and FDF03-S2. The proteins are involved in the
 CC regulation, or development, of haematopoietic cells. Antibodies specific
 CC for antigenic components of the proteins can be used to detect the
 CC components in samples. The proteins can also be used to screen for
 CC candidate therapeutic agents. The monocyte-derived proteins and
 CC polynucleotides can be used for diagnosis of diseases related to an
 CC increase, or decrease, in the number of monocytes in a tissue or lymph
 CC system, such as monocyte hyperplasia, tissue or graft rejection,
 CC inflammation, or bacterial or viral infections. The proteins can also be
 CC used in the treatment of disorders associated with abnormal expression or
 CC signalling by a monocyte
 XX
 XX Sequence 230 AA;
 SQ
 Query Match 73.9%; Score 1176.5; DB 3; Length 230;
 Best Local Similarity 75.9%; Pred. No. 4.2e-88;
 Matches 230; Conservative 0; Mismatches 0; Indels 73; Gaps 1;

```

QY 1 MGRPLLLPPLPPLPAPLQPSGSGTSGPSYLYGVTPQKHLASMGSGVEIPPSFYYPWE 60
DB 1 MGRPLLLPPLPPLPAPLQPSGSGTSGPSYLYGVTPQKHLASMGSGVEIPPSFYYPWE 60
QY 61 LATAPDVIRISWRGRGHFGQSFYSTRPPSIHKDYVNLFLNWTBQKSGFLRISNLQKODQ 120
DB 61 LATAPDVIRISWRGRGHFGQSFYSTRPPSIHKDYVNLFLNWTBQKSGFLRISNLQKODQ 120
QY 121 SVYFCRVELDTRSSGROQWOSIEGTKLSTQAVTTTQRPSSMTTWRLSSTTTTGLAV 180
DB 121 SVYFCRVELDTRSSGROQWOSIEGTKLSTQ----- 151
QY 181 TQGRKRSDSWHISLETAVGVAVAATVVLGIMLGLICLLRMRKRGQORTKATTPAREPQ 240
DB 152 -----GQORTKATTPAREPQ 167
QY 241 NTEEPYENIRNEGQNTDPKLNPKODGIVYASLALSSSTSPRAPPSHRPLKSPONETLYSV 300
DB 168 NTEEPYENIRNEGQNTDPKLNPKODGIVYASLALSSSTSPRAPPSHRPLKSPONETLYSV 227
QY 301 LKA 303
DB 228 LKA 230

RESULT 5
ADE95578
ID ADE95578 standard; protein: 230 AA.
XX AC ADE95578;
XX 12-FEB-2004 (first entry)
XX DE Human NOVX18a protein.
XX KM NOVX protein, biochemical stimulation; physiological stimulation;
KM cardiant; antiarteriosclerotic; hypotensive; cytosolic; anorectic;
KM antiinflammatory; antidiabetic; nephroprotective; dermatological;
KM immunosuppressive; anti-HIV; antiinflammatory; neuroprotective;
KM noctropic; antipsoriatic; antiparkinsonian; antiaslathetic; neuroleptic;
KM antidiabetic; antiallergic; gynaecological; gene therapy; vaccine;
KM NOVX-associated disorder; cardiomyopathy; atherosclerosis; hypertension;
KM cancer; obesity; rheumatoid arthritis; diabetes; glomerulonephritis;
KM psoriasis; skin disorder; AIDS; inflammation; multiple sclerosis;
KM Alzheimer's disease; Parkinson's disease; asthma; schizophrenia;
KM depression; allergy; fertility disorder; NOVX18a.
XX OS Homo sapiens.
XX PN MO2003050245-A2.
XX PD 19-JUN-2003.
XX PF 03-DEC-2002; 2002MO-US038594.
XX PR 05-DEC-2001; 2001US-033600P.
PR 07-DEC-2001; 2001US-038285P.
PR 12-DEC-2001; 2001US-0341346P.
PR 17-DEC-2001; 2001US-0341477P.
PR 17-DEC-2001; 2001US-0341540P.
PR 20-DEC-2001; 2001US-0342592P.
PR 27-DEC-2001; 2001US-0344297P.
PR 31-DEC-2001; 2001US-0344903P.
PR 17-APR-2002; 2002US-0373288P.
PR 15-MAY-2002; 2002US-0380981P.
PR 17-MAY-2002; 2002US-0381495P.
PR 28-MAY-2002; 2002US-0383534P.
PR 28-MAY-2002; 2002US-0383744P.
PR 29-MAY-2002; 2002US-0383829P.
PR 29-MAY-2002; 2002US-03840024P.
PR 07-AUG-2002; 2002US-0401788P.
PR 26-AUG-2002; 2002US-0406353P.
PR 31-OCT-2002; 2002US-040401788.

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PR 02-DEC-2002; 2002US-00406353.
XX (CURA-) CURAGEN CORP.
PA
XX A1sbrook JP, Anderson DW, Boldog FL, Burgess CE, Chilikuru RA;
PI Binger SR, Gerlach VL, Gorman L, Gould-Rothberg BE, Guo X;
PI Jeffers ME, Ji W, Li L, Malpankar UM, Miller CE, Murphy R;
PI Paturajan M, Peyman JA, Rastelli L, Rieger DK, Shenoy SG;
PI Smithson G, Stirling G, Taupler RJ, Voss EZ, Zhong H, Zhong M;
DR WPI, 2003-513974/48.
DR N-P-SDB; ADE95577.
XX
PT New NOVX polypeptides and nucleic acids, useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
PT atherosclerosis or diabetes, and in chromosome mapping, tissue typing or
PT pharmacogenomics.
PT
XX Claim 2; SEQ ID NO 110; 211pp; English.
XX
XX This invention relates to novel NOVX proteins, and the DNA sequence which
XX encode them, having properties related to stimulation of biochemical or
XX physiological responses in a cell, a tissue, an organ or an organism.
XX Compounds which modulate the proteins of the invention may have cardiant,
XX antiarteriosclerotic, hypotensive, cytosolic, anorectic, antidiabetic,
XX antiallergic, antidiabetic, nephroprotective, dermatological,
XX immunosuppressive, anti-HIV, antiinflammatory, neuroprotective,
XX noctropic, antipsoriatic, antiparkinsonian, antiaslathetic, neuroleptic,
XX antidiabetic, antiallergic or gynaecological activities. The DNA
XX sequences of the invention may be useful for gene therapy whilst the
XX protein sequences may allow the development of a vaccine. The protein is
XX useful in the manufacture of a medicament for treating a syndrome
XX associated with a human disease. The invention may be useful in
XX diagnosing, treating or preventing NOVX-associated disorders, for example
XX cardiomyopathy, atherosclerosis, hypertension, cancer, obesity,
XX rheumatoid arthritis, diabetes, glomerulonephritis, psoriasis, skin
XX disorders, AIDS, inflammation, multiple sclerosis, Alzheimer's disease,
XX Parkinson's disease, asthma, schizophrenia, depression, allergies or
XX fertility disorders. The nucleic acids may further be used as
XX hybridisation probes, in chromosome mapping, tissue typing, preventive
XX medicine, and pharmacogenomics. The present sequence is the amino acid
XX sequence of the human NOVX18a protein of the invention.
XX
SQ Sequence 230 AA:
Query Match 73.6%; Score 1171.5; DB 7; Length 230;
Best Local Similarity 75.6%; Pred. No. 1.1e-87;
Matches 229; Conservative 0; Mismatches 1; Indels 73; Gaps 1;
QY 1 MGRPLLLPPLPPLPAPLQPSGSGTSGPSYLYGVTPQKHLASMGSGVEIPPSFYYPWE 60
DB 1 MGRPLLLPPLPPLPAPLQPSGSGTSGPSYLYGVTPQKHLASMGSGVEIPPSFYYPWE 60
QY 61 LATAPDVIRISWRGRGHFGQSFYSTRPPSIHKDYVNLFLNWTBQKSGFLRISNLQKODQ 120
DB 61 LATAPDVIRISWRGRGHFGQSFYSTRPPSIHKDYVNLFLNWTBQKSGFLRISNLQKODQ 120
QY 121 SVYFCRVELDTRSSGROQWOSIEGTKLSTQAVTTTQRPSSMTTWRLSSTTTTGLAV 180
DB 121 SVYFCRVELDTRSSGROQWOSIEGTKLSTQ----- 151
QY 181 TQGRKRSDSWHISLETAVGVAVAATVVLGIMLGLICLLRMRKRGQORTKATTPAREPQ 240
DB 152 -----GQORTKATTPAREPQ 167
QY 241 NTEEPYENIRNEGQNTDPKLNPKODGIVYASLALSSSTSPRAPPSHRPLKSPONETLYSV 300
DB 168 NTEEPYENIRNEGQNTDPKLNPKODGIVYASLALSSSTSPRAPPSHRPLKSPONETLYSV 227
QY 301 LKA 303
DB 228 LKA 230

```


RESULT 6
ADE95580
ID ADE95580 standard; protein, 206 AA.
XX AC ADE95580;
XX
DT 12-FEB-2004 (first entry)
XX
XX Human NOVX18b protein.
DE
XX NOVX protein; biochemical stimulation; physiological stimulation;
KW cardiatic; antihypertensive; hypotensive; cytoskeletal; anorectic;
KW antihypertensive; antidiabetic; antidiabetic; nephrotropic; dermatological;
KW immunosuppressive; anti-HIV; antineoplastic; neuroprotective;
KW neurotropic; antiparkinsonian; antiparkinsonian; neuroleptic;
KW antidepressant; antiallergic; gynaecological; gene therapy; vaccine;
KW NOVX-associated disorder; cardiomyopathy; atherosclerosis; hypertension;
KW cancer; obesity; rheumatoid arthritis; diabetes; glomerulonephritis;
KW psoriasis; skin disorder; AIDS; inflammation; multiple sclerosis;
KW Alzheimer's disease; Parkinson's disease; asthma; schizophrenia;
KW depression; allergy; fertility disorder; NOVX18b.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Misc-difference 99
FT /label= OTHER
FT /note= "OTHER= May be substituted by Cys as a result of a
FT single nucleotide polymorphism"
FT Misc-difference 147
FT /label= OTHER
FT /note= "OTHER= May be substituted by Gly as a result of a
FT single nucleotide polymorphism"
FT Misc-difference 170
FT /label= OTHER
FT /note= "OTHER= May be substituted by Thr as a result of a
FT single nucleotide polymorphism"
XX
XX WO2003050245-A2.
XX
XX 19-JUN-2003.
XX
XX 03-DEC-2002; 2002WO-US038594.
XX
XX 05-DEC-2001; 2001US-0336600P.
XX 07-DEC-2001; 2001US-0338285P.
XX 12-DEC-2001; 2001US-0341346P.
XX 17-DEC-2001; 2001US-0341477P.
XX 17-DEC-2001; 2001US-0341540P.
XX 20-DEC-2001; 2001US-0342592P.
XX 27-DEC-2001; 2001US-0344297P.
XX 31-DEC-2001; 2001US-0344903P.
XX 17-APR-2002; 2002US-0373288P.
XX 15-MAY-2002; 2002US-0380981P.
XX 17-MAY-2002; 2002US-0381495P.
XX 28-MAY-2002; 2002US-0383534P.
XX 28-MAY-2002; 2002US-0383744P.
XX 29-MAY-2002; 2002US-0383829P.
XX 29-MAY-2002; 2002US-0384024P.
XX 07-AUG-2002; 2002US-0401788P.
XX 26-AUG-2002; 2002US-0406353P.
XX 31-OCT-2002; 2002US-00401788.
XX 02-DEC-2002; 2002US-00406353.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Alesbrook JP, Anderson DW, Boldog FL, Burgess CE, Chilikuru RA,
PI Edinger SR, Gerlach VL, Gorman L, Gould-Rothberg BE, Guo X,
PI Jeffers ME, Ji W, Li L, Malyankar UM, Miller CE, Murphy R,
PI Patursajan M, Peyman JA, Rascelli L, Rieger DK, Shenoy SG,
PI Smithson G, Starling G, Taupier RJ, Voss EZ, Zhong H, Zhong M;

DR WPI; 2003-513974/48.
XX N-PSDB; ADE95579.
XX
XX New NOVX polypeptides and nucleic acids, useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
PT atherosclerosis or diabetes, and in chromosome mapping, tissue typing or
XX pharmacogenomics.
XX
PS Claim 2; SEQ ID NO 112; 211pp; English.
XX
XX This invention relates to novel NOVX proteins, and the DNA sequence which
XX encode them, having properties related to stimulation of biochemical or
XX physiological responses in a cell, a tissue, an organ or an organism.
XX Compounds which modulate the proteins of the invention may have cardiatic,
XX antihypertensive, hypotensive, cytoskeletal, anorectic, antineumatic,
XX antidiabetic, antiparkinsonian, antiparkinsonian, neuroprotective,
XX immunosuppressive, anti-HIV, antineoplastic, neuroleptic,
XX neurotropic, antiparkinsonian, antiparkinsonian, neuroleptic,
XX antidepressant, antiallergic or gynaecological activities. The DNA
XX sequences of the invention may be useful for gene therapy whilst the
XX protein sequences may allow the development of a vaccine. The protein is
XX useful in the manufacture of a medicament for treating a syndrome
XX associated with a human disease. The invention may be useful in
XX diagnosing, treating or preventing NOVX-associated disorders, for example
XX cardiomyopathy, atherosclerosis, hypertension, cancer, obesity,
XX rheumatoid arthritis, diabetes, glomerulonephritis, psoriasis, skin
XX disorders, AIDS, inflammation, multiple sclerosis, Alzheimer's disease,
XX Parkinson's disease, asthma, schizophrenia, depression, allergies or
XX fertility disorders. The nucleic acids may further be used as
XX hybridisation probes, in chromosome mapping, tissue typing, preventive
XX medicine, and pharmacogenomics. The present sequence is the amino acid
XX sequence of the human NOVX18b protein of the invention.
SQ Sequence 206 AA:

Query Match 63.5%; Score 1010.5; DB 7; Length 206;
Best Local Similarity 67.7%; Pred. No. 1.5e-74;
Matches 205; Conservative 0; Mismatches 1; Indels 97; Gaps 2;

QY 1 MGRPLLPPLLPPLPAFLQPSGSGSYLYGVTPKHLASMGSGVEIPSFYRWE 60
DB 1 MGRPLLPPLLPPLPAFLQPSGSGSYLYGVTPKHLASMGSGVEIPSFYRWE 60
QY 61 LATAPDVIRISMRGHFGQSFYSTRPSPHNDYNNRLPLNTEBOKSFLAISNLOKXDO 120
DB 61 LAT-----SIHNDYNNRLPLNTEBOKSFLAISNLOKXDO 96
QY 121 SVYFCRVELDTRSSGROOMOSIEGKLSITQAVTTTORPSSMTTWTMLSTTTTGLRV 180
DB 97 SVYFCRVELDTRSSGROOMOSIEGKLSITQ----- 127
QY 181 TQGRKRSDSWHISLETAVGAVAVTALGIMILGICLLMRRRRQGOQTKATPARBEFQ 240
DB 128 -----GQQTAKATPARBEFQ 143
QY 241 NTEEPYENIRNEGQTPDKLPKNDGIVYASLASSSTSPAPSPSHRLKSPQNETLYSV 300
DB 144 NTEEPYENIRNEGQTPDKLPKNDGIVYASLASSSTSPAPSPSHRLKSPQNETLYSV 203
QY 301 LKA 303
DB 204 LKA 206

RESULT 7
AAV08015
ID AAV08015 standard; protein, 226 AA.
XX
XX AAV08015;
XX
XX 08-JUL-1999 (first entry)
XX
XX Human LSP-1 protein.
DE

XX	LSP-1, signal peptide; leucocyte-specific protein-1; PA-1, TAP-1; cancer;
KM	proliferin analogue I; thrombopoietin analogue protein 1; anticancer;
KM	antiangiogenic; anticancer; anti-inflammatory; anti-thrombocytopenic;
KM	anti-arthritic; signal transduction; inflammatory; disease; growth;
KM	proliferation; differentiation; cell survival; angiogenesis; diagnosis;
KM	haematopoietic stem cell; erythroid precursor; megakaryocytopoiesis;
KM	thrombopoiesis; prognosis; treatment; chromosome mapping; tissue typing;
KM	forensic; arthritis; thrombocytopenia; bone marrow transplant; infection;
KM	intravascular coagulation; iron deficiency; HIV; human.
XX	
OS	Homo sapiens.
XX	
XX	WO9918243-A1.
PD	15-APR-1999.
XX	
XX	06-OCT-1998; 98MO-US021151.
PF	
XX	06-OCT-1997; 97US-0061143P.
PR	
XX	06-OCT-1997; 97US-0061149P.
PR	
XX	06-OCT-1997; 97US-0061159P.
PR	
XX	08-JAN-1998; 98US-00004206P.
PR	
XX	22-JAN-1998; 98US-00010674.
PR	
XX	27-JAN-1998; 98US-00014347.
PA	(MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
XX	
XX	Pan Y, Gearing DP, McCarthy SA;
PI	
XX	WPI, 1999-264042/22.
DR	
XX	N-PSDB; AAX37558.
PT	
XX	Signal-peptide containing proteins that modulate cellular processes.
PS	
XX	Claim 2; Fig 1; 124pp; English.
XX	
CC	This invention describes the isolation of nucleic acids encoding the
CC	signal-peptide-containing molecules leucocyte-specific protein-1 (LSP-1),
CC	proliferin analog I (PA-I) and thrombopoietin analog protein 1 (TAP-1).
CC	These proteins have antiangiogenic, anticancer, anti-inflammatory, anti-
CC	arthritic and anti-thrombocytopenic activity. The products of the
CC	invention and their modulators are involved in signal transduction,
CC	inflammatory responses, growth, proliferation, differentiation and
CC	survival of cells; angiogenesis; maturation of haematopoietic stem cells
CC	and erythroid precursors megakaryocytopoiesis and thrombopoiesis.
CC	Antibodies, or other binding agents, specific for the products of the
CC	invention are useful for diagnosis, prognosis and monitoring of treatment
CC	of diseases. Other uses include chromosome mapping, identification of
CC	individuals (tissue typing) and in forensic studies. LSP-1, PA-I and TAP-
CC	I proteins and nucleic acids are modulators of cellular processes,
CC	particularly they are used to treat or prevent diseases associated with
CC	deregulation of angiogenesis, immune responses and haematopoiesis, e.g.
CC	cancer, arthritis (and other inflammatory diseases), thrombocytopenia
CC	(caused by cancer treatment, bone marrow transplant, human immune
CC	deficiency virus infection etc.), intravascular coagulation, iron
CC	deficiency etc
XX	
XX	
SO	Sequence 226 AA;
	Query Match 61.2%; Score 973.5; DB 2; Length 226;
	Best Local Similarity 82.5%; Pred. No. 1.8e-71;
	Matches 188; Conservative 14; Mismatches 17; Indels 9; Gaps 2
QY	1 MGRPLLLPLPLLLPPAPLPSPGSGSGSYGYCTTOPKHLASASMGSGVEIPFSYYPWE 60
DB	1 MGRPLLLPLLLLOPAPLPSPGSGSGSYGYCTOPKHLASASMGSGVEIPFSYYPWE 60
QY	61 LATAPDVAISWGRGFHSGSFYSTRPSPSIHKXYNRLPLNMTREGKSGGLRISNIOKOPQ 120
DB	61 LATAPDVAISWGRGFHSGSFYSTRPSPSIHKXYNRLPLNMTREGKSGGLRISNIRKEQ 120
QY	121 SVYFQRVEIDTRSSGRQOMQSIETKRLSITQAVTTTQORPSSMTTWRLSITTTTGLRV 180

DB	121	SVYCRVELDTRRSGRGOLOSIKETKLTITQAVTT-----TTTMRPSSTITTAGLRV	172
QY	181	TGGRRSDSWHISLETAVGVAVAATVIGIMILGICLLR-WRRKQGO 227	
DB	173	TESKSHSESWHLSDTAIRVALAAVAALVKVILGLICLLMWRRRKGR 220	
RESULT 8			
AAAB07447			
ID	AAAB07447	standard; protein; 226 AA.	
XX	AAAB07447;		
AC	20-OCT-2000	(first entry)	
DT			
XX			
XX			
DE		A human monocyte-derived protein FDF03-S2.	
XX			
KW		Human; monocyte-derived protein; FDF03; FDF03delatm; FDF03-S1;	
KW	FDF03-M14; FDF03-S2;	haematopoietic cell; monocyte hyperplasia;	
KW		tissue rejection; inflammation; infection.	
XX			
OS		Homo sapiens.	
XX			
Key		Location/Qualifiers	
FT	Peptide	1..17	
FT		/note= "signal sequence"	
FT	Protein	18..226	
FT		/note= "mature protein"	
XX			
PN		WO200040721-A1.	
PD			
XX		13-JUL-2000.	
PF		29-DEC-1999; 99WO-US030004.	
PR		31-DEC-1998; 98US-00223919.	
PR		31-DEC-1998; 98US-00224604.	
XX			
PA		(SCHE) SCHERING CORP.	
XX			
PI		Bates E, Fournier N, Chaulus L, Garrone P;	
XX			
DR		WPI; 2000-465984/40.	
XX		N-PSDB; AAA58818.	
PT		Novel monocyte-derived polypeptides and polynucleotides, used to diagnose	
PT		diseases associated with changes in monocyte numbers, e.g. bacterial or	
PT		viral infections.	
XX			
PS		Claim 1; Page 41-42; 45p; English.	
XX			
CC		The present sequence represents a human monocyte-derived protein. The	
CC		specification describes monocyte-derived proteins FDF03, FDF03delatm,	
CC		FDF03-S1, FDF03-M14, and FDF03-S2. The proteins are involved in the	
CC		regulation, or development, of haematopoietic cells. Antibodies specific	
CC		for antigenic components of the proteins can be used to detect the	
CC		components in samples. The proteins can also be used to screen for	
CC		candidate therapeutic agents. The monocyte-derived proteins and	
CC		polynucleotides can be used for diagnosis of diseases related to an	
CC		increase, or decrease, in the number of monocytes in a tissue or lymph	
CC		system, such as monocyte hyperplasia, tissue or graft rejection,	
CC		inflammation, or bacterial or viral infections. The proteins can also be	
CC		used in the treatment of disorders associated with abnormal expression or	
CC		signalling by a monocyte	
XX			
XX			
SQ		Sequence 226 AA;	
Query Match	61.2%;	Score 973.5; DB 3; Length 226;	
Best Local Similarity	82.5%;	Pred. No. 1.8e-71;	
Matches 188;	Conservative 14;	Mismatches 17; Indels 9; Gaps 2	
QY	1	MGRPLLPFLPFLPPAFLPQSGSTGSPSYLVGVTQPKHLASMGSGVEIPFSFYRWE	60

Db 1 MGRPLLLPPLLLLPAPLQPGSGSPSYLVGTQPKHLSASMGSSVELPFSTFYWE 60
Qy 61 LATAPDVRISWRKGFHFGQSFYSTRPSPSIHKDYNRFLFNWTEGQSGFLRISNLKQDQ 120
Db 61 LATAPDVRISWRKGFHFGQSFYSTRPSPSIHKDYNRFLFNWTEGQSGFLRISNLKQDQ 120
Qy 121 SVYFCRVELDTRRSSGRQOQOSIEGFKLSITQAVTTTTPRPSMTTWRLSSTTTTGLRV 180
Db 121 SVYFCRVELDTRRSSGRQOQOSIEGFKLSITQAVTTTTPRPSMTTWRLSSTTTTGLRV 172
Qy 181 TQGRKRDSDWHISLETAVGAVAVATVGLIMILGICLLR-WRRKGGQ 227
Db 173 TESKGSSESWHLSLDTAIRVALAVAVLKTIVILGILLMLMRRRKGSR 220

RESULT 9
AAW80407 standard; protein; 226 AA.

AC AAW80407;
DT 25-MAR-2003 (revised)
DT 13-JAN-1999 (first entry)
XX
DE A secreted protein encoded by clone d139_9.

XX Secreted protein; immune stimulating; suppressing;
XX haematopoiesis regulating activity; tissue growth activity; activin;
XX inhibin activity; chemotactic; chemokinetic activity; haemostatic;
XX thrombolytic activity; anti-inflammatory activity; cadherin;
XX tumour invasion suppressor activity; tumour inhibition activity.

XX Homo sapiens.
XX MO9844113-A1.

XX PD 08-OCT-1998.

XX PF 27-MAR-1998; 98MO-US006176.

XX PR 28-MAR-1997; 97US-00823330.

XX PR 25-MAR-1998; 98US-00047661.

XX PA (GEM) GENETICS INST INC.

XX PI Jacobs K, McCoy JM, Lavallie ER, Racie LA, Merberg D, Treacy M;
XX Spaulding V, Agostino MJ;
XX

XX WP1; 1998-542703/46.
XX N-PSDB; AAV63191.

XX New isolated polynucleotide(s) and secreted proteins - are obtained from
XX human cDNA libraries prepared from adult testes, foetal brain, adult
XX brain, adult blood and placenta.

XX Claim 19; Page 76-77; 124p; English.

XX The present sequence represents a secreted protein. The nucleic acid
XX sequence is isolated from a human adult testes cDNA library using probe
XX AAV631202. The polypeptide may have biological activities such as e.g.
XX nutritional activity, immune stimulating or suppressing activity,
XX haematopoiesis regulating activity, tissue growth activity,
XX activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
XX activity, thrombolytic activity, receptor/ligand activity, anti-inflammatory
XX activity, cadherin/tumour invasion suppressor activity, tumour inhibition
XX activity or other activities. (Updated on 25-MAR-2003 to correct PR
XX field.)

XX Sequence 226 AA;

Query Match 60.8%; Score 967.5; DB 2; Length 226;
Best Local Similarity 82.0%; Pred. No. 5.5e-71;

Matches 187; Conservative 14; Mismatches 18; Indels 9; Gaps 2;
Qy 1 MGRPLLLPPLLLLPAPLQPGSGSPSYLVGTQPKHLSASMGSSVELPFSTFYWE 60
Db 1 MGRPLLLPPLLLLPAPLQPGSGSPSYLVGTQPKHLSASMGSSVELPFSTFYWE 60
Qy 61 LATAPDVRISWRKGFHFGQSFYSTRPSPSIHKDYNRFLFNWTEGQSGFLRISNLKQDQ 120
Db 61 LATAPDVRISWRKGFHFGQSFYSTRPSPSIHKDYNRFLFNWTEGQSGFLRISNLKQDQ 120
Qy 121 SVYFCRVELDTRRSSGRQOQOSIEGFKLSITQAVTTTTPRPSMTTWRLSSTTTTGLRV 180
Db 121 SVYFCRVELDTRRSSGRQOQOSIEGFKLSITQAVTTTTPRPSMTTWRLSSTTTTGLRV 172
Qy 181 TQGRKRDSDWHISLETAVGAVAVATVGLIMILGICLLR-WRRKGGQ 227
Db 173 TESKGSSESWHLSLDTAIRVALAVAVLKTIVILGILLMLMRRRKGSR 220

RESULT 10
ABP61825 standard; protein; 226 AA.

AC ABP61825;
DT 04-OCT-2002 (first entry)
XX
DT

XX Human polypeptide SEQ ID NO 179.

XX Human; cytosolic; antirheumatic; antiarthritic; vulnery; analgesic;
XX antiinflammatory; antibacterial; immunosuppressive; antiparkinsonian;
XX neuroprotective; nocotropic; osteopathic; haemostatic; vasotropic;
XX antidiabetic; antidiabetic; antidiabetic; antidiabetic;
XX immunostimulant; antiparalytic; secreted protein; transmembrane protein;
XX cytokine; cell proliferation; cell differentiation; autoimmune disease;
XX stem cell; growth factor; nervous system disease; neuropathy;
XX Alzheimer's disease; Parkinson's disease; Huntington's disease;
XX osteoporosis; severe combined immunodeficiency; SCID; infection;
XX multiple sclerosis; rheumatoid arthritis; gene therapy.

XX Homo sapiens.

XX US2002065394-A1.

XX PD 30-MAY-2002.

XX PF 22-DEC-2000; 2000US-00745763.

XX PR 18-MAR-1998; 98US-00040963.

XX PA (JACO) JACOBS K.
XX PA (MCCO) MCCOY J M.
XX PA (LAVA) LAVALLIE E R.
XX PA (COLL) COLLINS-RACIE L A.
XX PA (EVAN) EVANS C.
XX PA (MERB) MERBERG D.
XX PA (TREAC) TREACY M.
XX PA (SPAUV) SPAULDING V.
XX

XX Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;
XX Merberg D, Treacy M, Spaulding V;
XX

XX Novel secreted or transmembrane protein and polynucleotide encoding the
XX protein, useful for diagnosis and treatment of neurological disorders,
XX cancer, autoimmune diseases, bone disorders and lung or liver fibrosis.

XX Claim 136; Page 159; 284p; English.

XX The invention relates to human secreted or transmembrane protein (I),
XX their fragments and is encoded by specific complementary deoxyribonucleic

CC acid (cDNA) inserts (II), where the protein is substantially free from
 CC other mammalian proteins. (I) are useful for preventing, treating or
 CC ameliorating a medical condition, especially immunological treatment or
 CC prevention of tumours. (I) exhibits activity relating to angiogenesis,
 CC cytokine, cell proliferation, cell differentiation, antiinflammatory,
 CC stem cell growth factor activity and activin or inhibin-related
 CC activities. (I) can be used to manipulate stem cells in culture to give
 CC rise to neuroepithelial cells that can be used to augment or replace
 CC cells damaged by illness, autoimmune disease, accidental damage or
 CC genetic disorders. (I) induces the proliferation of neural cells and
 CC regeneration of nerve and brain tissue and is useful for the treatment of
 CC central and peripheral nervous system diseases and neuropathies, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis. (I) is involved in chemotactic or chemokinetic
 CC activity, regulation of haemopoiesis and is useful for treating myeloid
 CC or lymphoid cell disorders, platelet disorders such as thrombocytopenia
 CC and for regeneration of bone, cartilage, tendon, ligament and/or nerve
 CC tissue growth and in tissue repair, healing of burns, incisions, ulcers,
 CC for treating osteoporosis, osteoarthritis, bone degenerative disorders or
 CC periodontal disease. (I) is also useful for gut protection or
 CC regeneration and treatment of lung or liver fibrosis, reperfusion injury
 CC in various tissues, various immune deficiencies and disorders including
 CC severe combined immunodeficiency (SCID), bacterial and fungal infections,
 CC autoimmune disorders e.g. multiple sclerosis, rheumatoid arthritis,
 CC diabetes mellitus, myasthenia gravis, allergic reactions and conditions,
 CC such as asthma or other respiratory problems. (II) is useful to express
 CC recombinant protein, as markers for tissues in which the corresponding
 CC protein is preferentially expressed and in gene therapy. The present
 CC sequence is that of a polypeptide of the invention

XX Sequence 226 AA;

SO Query Match 60.8%; Score 967.5; DB 5; Length 226;
 Best Local Similarity 82.0%; Pred. No. 5.5e-71;
 Matches 187; Conservative 14; Mismatches 18; Indels 9; Gaps 2;

QY 1 MGRPLLLPLPLLLPAPLPPSGSTGSPSYLYGVTPKHLASMGSGVEIPPSFYYPWE 60
 Db 1 MGRPLLLPLLLPLLPAPLPPSGSTGSPSYLYGVTPKHLASMGSGVEIPPSFYYPWE 60
 QY 61 LATAPDVRIISWRGHHFGSGFYSTRPPSIHKDYVNRFLFWMTGQSGFLRISNLKQDQ 120
 Db 61 LATAPDVRIISWRGHHFGSGFYSTRPPSIHKDYVNRFLFWMTGQSGFLRISNLKQDQ 120
 QY 121 SYVFCRVELDTRSSGRQOQSIKGTLTTOAVTTTTPRPSMTTWRSLSTTTTGLRV 180
 Db 121 SYVFCRVELDTRSSGRQOQSIKGTLTTOAVTTTTPRPSMTTWRSLSTTTTGLRV 172
 QY 181 TOGKRSDSMHISLETAVGVAVAVTVLIGIMLGLICLLR-WRRRKGOQ 227
 Db 173 TESKGHSESWHLSDTAIRVALAVAVLKVITLGLCLLMWRRRKGR 220

RESULT 11
 AAB07445 standard; protein; 227 AA.

XX AAB07445;

DT 20-OCT-2000 (first entry)

DE A human monocyte-derived protein FDF03-S1.

XX Human, monocyte-derived protein; FDF03; FDF03deltaTM, FDF03-S1;
 KM FDF03-M14; FDF03-S2; haematopoietic cell; monocyte hyperplasia;
 KM tissue rejection; inflammation; infection.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..17
 FT Protein /note="signal sequence"
 FT 18..227

FT /note="mature protein"

PN MO200040721-A1.

PD 13-JUL-2000.

PF 29-DEC-1999; 99WO-US030004.

PR 31-DEC-1998; 98US-00223919.

PR 31-DEC-1998; 98US-00224604.

PA (SCHE) SCHERRING CORP.

PI Bates E, Fournier N, Chauvis I, Garrone P;

DR WPI; 2000-465984/40.

DR N-PSDB; AAM58816.

PT Novel monocyte-derived polypeptides and polynucleotides, used to diagnose
 PT diseases associated with changes in monocyte numbers, e.g. bacterial or
 PT viral infections.

PS Claim 1; Page 37-38; 45pp; English.

XX The present sequence represents a human monocyte-derived protein. The
 CC specification describes monocyte-derived proteins FDF03, FDF03deltaTM,
 CC FDF03-S1, FDF03-M14, and FDF03-S2. The proteins are involved in the
 CC regulation, or development, of haematopoietic cells. Antibodies specific
 CC for antigenic components of the proteins can be used to detect the
 CC components in samples. The proteins can also be used to screen for
 CC candidate therapeutic agents. The monocyte-derived proteins and
 CC polynucleotides can be used for diagnosis of diseases related to an
 CC increase, or decrease, in the number of monocytes in a tissue or lymph
 CC system, such as monocyte hyperplasia, tissue or graft rejection, CC
 CC inflammation, or bacterial or viral infections. The proteins can also be
 CC used in the treatment of disorders associated with abnormal expression or
 CC signalling by a monocyte

SO Sequence 227 AA;

Query Match 60.2%; Score 958; DB 3; Length 227;
 Best Local Similarity 80.8%; Pred. No. 3.3e-70;
 Matches 185; Conservative 15; Mismatches 19; Indels 10; Gaps 2;

QY 1 MGRPLLLPLPLLLPAPLPPSGSTGSPSYLYGVTPKHLASMGSGVEIPPSFYYPWE 60
 Db 1 MGRPLLLPLLLPLLPAPLPPSGSTGSPSYLYGVTPKHLASMGSGVEIPPSFYYPWE 60
 QY 61 LATAPDVRIISWRGHHFGSGFYSTRPPSIHKDYVNRFLFWMTGQSGFLRISNLKQDQ 120
 Db 61 LATAPDVRIISWRGHHFGSGFYSTRPPSIHKDYVNRFLFWMTGQSGFLRISNLKQDQ 120
 QY 121 SYVFCRVELDTRSSGRQOQSIKGTLTTOAVTTTTPRPSMTTWRSLSTTTTGLRV 180
 Db 121 SYVFCRVELDTRSSGRQOQSIKGTLTTOAVTTTTPRPSMTTWRSLSTTTTGLRV 172
 QY 181 TOGKRSDSMHISLETAVGVAVAVTVLIGIMLGLICLLR-WRRRKGOQ 227
 Db 173 TESKGHSESWHLSDTAIRVALAVAVLKVITLGLCLLMWRRRKGR 221

RESULT 12

ABU89824 standard; protein; 227 AA.

XX ABU89824;

DT 10-JUL-2003 (first entry)

DE TNF-receptor associated factor 5 (TRAF5) interacting protein #4.

XX Human; cytostatic; DAPK3-Agonist; DAPK3-Antagonist; cancer;
 KM TNF-receptor associated factor 5 interacting protein;

KW tumour necrosis factor associated factor 5 interacting protein;
 KW TRAF5 interacting protein.
 OS Homo sapiens.
 PN MO2003031571-A2.
 XX 17-APR-2003.
 PD 02-OCT-2002; 2002WO-US031357.
 PF 05-OCT-2001; 2001US-0327454P.
 PR 09-OCT-2001; 2001US-0327917P.
 PR 09-OCT-2001; 2001US-0328029P.
 PR 09-OCT-2001; 2001US-0328056P.
 PR 12-OCT-2001; 2001US-0328849P.
 PR 15-OCT-2001; 2001US-0329414P.
 PR 17-OCT-2001; 2001US-0330142P.
 PR 22-OCT-2001; 2001US-0341058P.
 PR 24-OCT-2001; 2001US-0343575P.
 PR 29-OCT-2001; 2001US-0343575P.
 PR 01-NOV-2001; 2001US-0346357P.
 PR 25-JUN-2002; 2002US-0391342P.
 PR 01-OCT-2002; 2002US-00262445.
 XX (CURA-) CURAGEN CORP.
 PA Alobrook JP, Burgess CE, Catterton E, Chant JS, Chaudhuri A;
 P1 Edinger SR, Gerlach VL, Giot L, Gorman L, Guo X, Kexuda R;
 P1 Mezes PS, Miller I, Oei CE, Paturajan M, Rieger DK, Spytek KA;
 P1 Taupier RJ, Zernusen BD, Zhong H, Zhong M;
 XX WPI; 2003-381704/36.
 DR N-PSDB; ACP90240.
 XX New DAPK3 polypeptide, useful for preparing a composition for treating or
 PT preventing e.g., cancer.
 PT Example 20F; Page 242; 253pp; English.
 XX The invention describes an isolated polypeptide comprising any of 33 90-
 CC 1273 amino acid sequences (I) given in the specification or its mature
 CC form, a sequence that is at least 95 % identical to (I), or a sequence
 CC comprising one or more conservative substitutions in the amino acid
 CC sequence of (I). The polypeptide is useful for preparing a composition
 CC for treating or preventing e.g., cancer. This is the amino acid sequence
 CC of a tumour necrosis factor (TNF)-receptor associated factor 5 (TRAF5)
 CC interacting protein associated with the identification of novel human
 CC proteins and their functions
 XX Sequence 227 AA;
 SQ
 Query Match 60.2%; Score 958; DB 6; Length 227;
 Best Local Similarity 80.8%; Pred. No. 3.3e-70;
 Matches 185; Conservative 15; Mismatches 19; Indels 10; Gaps 2;
 Oy 1 MGRPLLLPPLLLPAPLQPSGSGSPSYLYGVTPKHSASMGSGVEIPFSFYWE 60
 Db 1 MGRPLLLPPLLLPAPLQPSGSGSPSYLYGVTPKHSASMGSGVEIPFSFYWE 60
 Oy 61 LATAPDVIRISWRGHFGOSFYSTRPSIHQYVNRLLPMTGEGSGFLIRISNLQKQDQ 120
 Db 61 LATAPDVIRISWRGHFGOSFYSTRPSIHQYVNRLLPMTGEGSGFLIRISNLQKQDQ 120
 Oy 121 SVYFGRVELDTRSSGRQMOQSIETKLSITQAVTTTTPRPSMTTWTWRLSTTTTGLRV 180
 Db 121 SVYFGRVELDTRSSGRQMOQSIETKLSITQAVTTTTPRPSMTTWTWRLSTTTTGLRV 180
 Oy 181 TQGRKRSQSMHSLSTAVGAVAVVVLGIMTIGLICLR--WRRKQDQ 227
 Db 173 TESKSHSSEWHLSDTAIRVALAVLVLTVTIIGLICLLILMWRRKRSR 221

RESULT 13
 ID AAW63682
 AC AAW63682 standard; protein; 291 AA.
 XX AAW63682;
 XX 24-SEP-1998 (first entry)
 DT Human secreted protein 2.
 DE
 XX Secreted protein; human; cell proliferation; cytokine activity;
 KW tissue growth; cellular differentiation; regeneration; activin; inhibin;
 KW chemoattract; haemostatic; thrombolytic; tumour inhibition;
 KW anti-inflammatory activity; biomarker.
 XX Homo sapiens.
 OS MO9825959-A2.
 PN 18-JUN-1998.
 PD 11-DEC-1997; 97WO-US022787.
 PF 11-DEC-1997; 96US-0032757P.
 PR 11-DEC-1996; 96US-0032757P.
 XX (CHIR) CHIRON CORP.
 PA Escobedo J, Hu Q, Garcia P, Williams LT, Kothakota S;
 P1 WPI; 1998-348453/30.
 DR N-PSDB; AAV43602.
 XX Secreted human polypeptides - having cytokine, cell proliferation or
 PT differentiation, activin or inhibin, tumour inhibition or anti-
 PT inflammatory activities.
 XX Claim 1; Page 49-50; 78pp; English.
 XX This represents a human secreted protein. The specification provides
 CC secreted protein sequences (AAW63681 to AAW63699) encoded by the nucleic
 CC acid sequences shown in AAV43601 to AAV43619. The invention provides a
 CC method of identifying a secreted polypeptide which is modified by rough
 CC microsomes. The secreted proteins can be used in assays to determine
 CC biological activities, such as cytokine, cell proliferation, or cellular
 CC differentiation activities, tissue growth or regeneration, activin or
 CC inhibin activity, chemotactic or chemokinetic activity, haemostatic or
 CC thrombolytic activity, receptor/ligand activity, tumour inhibition, or
 CC anti-inflammatory activity. The proteins can also be used as biomarkers,
 CC to identify tissues or cell types which express the proteins, or a stage-
 CC or disease-specific alteration in protein expression. They can be used in
 CC protein interaction assays, to identify ligands or binding proteins.
 CC Compounds which affect the biological activities of the secreted proteins
 CC or their ability to interact with specific ligands can be identified
 CC using the proteins in screening assays. The proteins and antibodies that
 CC bind specifically to the protein can also be used to design diagnostic
 CC tests and therapeutic compositions for diseases which may be associated
 CC with altered expression of these proteins. Fusion proteins comprising,
 CC e.g., signal sequences or transmembrane domains of the proteins can be
 CC used to target other protein domains to cellular membrane or they can be
 CC secreted extracellularly
 XX Sequence 291 AA;
 SQ
 Query Match 60.2%; Score 958; DB 2; Length 291;
 Best Local Similarity 80.8%; Pred. No. 4.5e-70;
 Matches 185; Conservative 15; Mismatches 19; Indels 10; Gaps 2;
 Oy 1 MGRPLLLPPLLLPAPLQPSGSGSPSYLYGVTPKHSASMGSGVEIPFSFYWE 60
 Db 65 MGRPLLLPPLLLPAPLQPSGSGSPSYLYGVTPKHSASMGSGVEIPFSFYWE 124
 Oy 61 LATAPDVIRISWRGHFGOSFYSTRPSIHQYVNRLLPMTGEGSGFLIRISNLQKQDQ 120

DB 125 LAIVPNVRISMRRGHFGHGSFYSTRPPSIHKDYVNRFLNMTGQESGFLRISNLRKEQD 184
 QY 121 SYVFCRVELDTRSSGRQOMQSIETKLSITQAVTTTQRSSMTTWRRISSTTTTGLRV 180
 DB 185 SYVFCRVELDTRSSGRQOMQSIETKLTITQAVTT-----TTWRRPSSTTTTIGLRV 236
 QY 181 TQGRKRSDSMHSLETFAGVAVAVTVLGMILGICLLR--WRRRKQD 227
 DB 237 TQSGHSESMHSLDTPAIRVALAVAVLKVITLGLCLLLMMWRRRKSR 285

RESULT 14
 ID ABB12010 standard; peptide; 326 AA.
 XX
 AC ABB12010;
 XX
 DT 11-JAN-2002 (first entry)
 XX
 DE Human secreted protein homologue, SEQ ID NO:2380.
 XX
 KW Human; cytokine; cell proliferation; cell differentiation; growth factor;
 KW haematopoietic regulation; tissue growth; immunomodulator; activin;
 KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
 KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
 KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
 KW chronic inflammatory condition; proliferative retinopathy;
 KW atherosclerosis; coronary heart disease; arterial ischaemia;
 KW bone disorder; osteoporosis; vascular growth disorder;
 KW tissue regeneration; wound healing; infection; immune disorder;
 KW cell culture; drug screening; gene therapy; antiinflammatory;
 KW antiaesthetic; antiarthritic; haemostatic; antiarteriosclerotic;
 KW cytostatic; osteopathic; vasotropic; cardiac; virucide; antibacterial;
 KW antifungal; vulnery; antitumor.
 XX
 OS Homo sapiens.
 XX
 PN MO200157188-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 05-FEB-2001; 2001MO-US0003800.
 XX
 PR 03-FEB-2000; 2000US-00496914.
 PR 27-APR-2000; 2000US-00560875.
 XX
 PA (HYSE-) HYSEO INC.
 XX
 PI Tang YT, Liu C, Drmanac RT;
 XX
 DR WPI; 2001-457740/49.
 DR N-PSDB; ABA09254.
 XX
 PT Human proteins and DNA encoding sequences useful for preventing, treating
 PT or ameliorating a medical condition in a mammalian subject e.g. arthritis
 PT and cancer.
 XX
 PS Claim 20; Page 295; 1963pp; English.
 XX
 CC Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
 CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
 CC invention also relates to vectors and recombinant host cells comprising a
 CC nucleotide of the invention, methods of producing the novel polypeptides,
 CC antibodies against the polypeptides, methods of detecting the nucleotides
 CC or polypeptides in a sample, and methods of identifying compounds which
 CC bind to polypeptides of the invention. Although novel, many of the
 CC polypeptides of the invention have homology to known proteins, thereby
 CC giving an insight into their probable biological activities, and hence
 CC potential therapeutic applications. The polypeptides of the invention may
 CC have various activities, including cytokine, cell proliferation or cell
 CC differentiation activities, stem cell growth factor activity;
 CC haematopoietic regulatory activity; tissue growth activity;
 CC immunomodulatory activity; activin- or inhibin-related activities;

CC chemotactic or chemokineic activities; haemostatic, thrombotic or
 CC thrombolytic activities; receptor or ligand activities; or may be
 CC involved in oncogenesis; cancer cell proliferation and metastasis.
 CC Depending on their biological activities, polypeptides and nucleotides of
 CC the invention are useful for preventing, treating or ameliorating medical
 CC conditions, e.g., by protein or gene therapy. Such conditions include
 CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
 CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
 CC proliferative retinopathy, atherosclerosis, coronary heart disease,
 CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
 CC vascular growth. Polypeptides involved with tissue regeneration and
 CC repair (or nucleic acids encoding them) may be used to promote wound
 CC healing (e.g., of burns, incisions and ulcers), while those with
 CC immunomodulatory activities may be used in the treatment of viral,
 CC bacterial and fungal infections in addition to immune disorders.
 CC Polypeptides with growth factor activity may be used in cell cultures to
 CC promote cell growth. For example, such polypeptides may be used to
 CC manipulate stem cells in culture to give rise to neuroepithelial cells
 CC that can be used to augment or replace cells damaged by illness,
 CC autoimmune disease or accidental damage. The polypeptides and nucleotides
 CC may also be used in the diagnosis of the above conditions, and in drug
 CC screening techniques. The present sequence represents a novel human
 CC polypeptide of the invention
 CC
 XX
 SQ Sequence 326 AA;
 XX
 Query Match 60.2%; Score 958; DB 4; Length 326;
 Best Local Similarity 80.8%; Pred. No. 5.3e-70;
 Matches 185; Conservative 15; Mismatches 19; Indels 10; Gaps 2;
 QY 1 MGRPLLPPLPPLLPAPLPQSGSTGSPSYLYGVTPRHLSASMGSEIIPSPFYYPWE 60
 DB 100 MGRPLLPPLPPLLPAPLPQSGSTGSPSYLYGVTPRHLSASMGSEIIPSPFYYPWE 159
 QY 61 LATAPVVRISMRRGHFGHGSFYSTRPPSIHKDYVNRFLNMTGQESGFLRISNLRKEQD 120
 DB 160 LAIVPNVRISMRRGHFGHGSFYSTRPPSIHKDYVNRFLNMTGQESGFLRISNLRKEQD 219
 QY 121 SYVFCRVELDTRSSGRQOMQSIETKLSITQAVTTTQRSSMTTWRRISSTTTTGLRV 180
 DB 220 SYVFCRVELDTRSSGRQOMQSIETKLTITQAVTT-----TTWRRPSSTTTTIGLRV 271
 QY 181 TQGRKRSDSMHSLETFAGVAVAVTVLGMILGICLLR--WRRRKQD 227
 DB 272 TQSGHSESMHSLDTPAIRVALAVAVLKVITLGLCLLLMMWRRRKSR 320

RESULT 15
 ID AAY87230
 XX
 AC AAY87230;
 XX
 DT 11-MAY-2000 (first entry)
 XX
 DE Human signal peptide containing protein HSP-7 SEQ ID NO:7.
 XX
 KW Human; signal peptide-containing protein; HSP; diagnosis; cancer;
 KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;
 KW antimicrobial; neuroprotective; cardiovascular; hepatotropic;
 KW antiaesthetic; gene therapy; cell proliferation; neurological disorder;
 KW reproductive disorder; developmental disorder; arteriosclerosis;
 KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;
 KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;
 KW Parkinson's disease; Huntington's disease; ovulatory defect;
 KW muscular dystrophy.
 XX
 OS Homo sapiens.
 XX
 PN MO200000610-A2.
 XX
 PD 06-JAN-2000.
 XX

PF	25-JUN-1999;	99WO-US014484.
XX		
PR	26-JUN-1998;	98US-0090762P.
PR	31-JUL-1998;	98US-0094963P.
PR	01-OCT-1998;	98US-0102686P.
PR	11-DEC-1998;	98US-0112129P.
XX		
PA	(INCY-) INCYTE PHARM INC.	
XX		
PI	Lal P, Teng YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MF; JL;	
PI	Akerblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman O;	
XX		
XX	WPI; 2000-160673/14.	
DR	N-PSDB; AA298115.	
XX		
PT	New human signal peptide-containing proteins useful in treatment,	
PT	prevention and diagnosis of e.g. cancer, inflammation and cardiovascular	
XX	disease.	

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OM protein - protein search, using sw model

Run on: June 1, 2005, 22:05:46 ; Search time 142 Seconds
(without alignments)
737.613 Million cell updates/sec

Title: US-10-777-524-2

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Listing first 45 summaries

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Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
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- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
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- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1591	100.0	303	10 US-09-774-381-58	Sequence 58, Appli
2	1591	100.0	303	14 US-10-290-631-2	Sequence 2, Appli
3	1591	100.0	303	16 US-10-780-043-2	Sequence 2, Appli
4	1591	100.0	303	16 US-10-777-524-2	Sequence 2, Appli
5	1591	100.0	303	17 US-10-777-521-2	Sequence 4, Appli
6	1176.5	79.9	230	16 US-10-780-043-4	Sequence 4, Appli
7	1171.5	73.6	230	15 US-10-309-290-110	Sequence 110, App
8	1010.5	63.5	206	15 US-10-309-290-112	Sequence 112, App
9	973.5	61.2	226	10 US-09-774-381-44	Sequence 44, Appli
10	973.5	61.2	226	16 US-10-780-043-10	Sequence 10, Appli
11	967.5	60.8	226	9 US-09-745-763-106	Sequence 106, App
12	958	60.2	227	15 US-10-262-445-128	Sequence 128, App
13	958	60.2	227	16 US-10-780-043-6	Sequence 6, Appli

14	958	60.2	291	9 US-09-935-390A-21	Sequence 21, Appli
15	958	60.2	326	15 US-10-276-774-2380	Sequence 2380, Ap
16	934	58.7	238	10 US-09-809-391-485	Sequence 485, App
17	934	58.7	238	10 US-09-882-171-485	Sequence 485, App
18	934	58.7	238	15 US-10-164-661-485	Sequence 8, Appli
19	821	51.6	175	16 US-10-780-043-8	Sequence 754, App
20	517	32.5	101	10 US-09-809-391-754	Sequence 754, App
21	517	32.5	101	10 US-09-882-171-754	Sequence 754, App
22	517	32.5	101	15 US-10-164-661-754	Sequence 754, App
23	411	25.8	224	10 US-09-866-050A-711	Sequence 711, App
24	411	25.8	99	14 US-10-290-631-4	Sequence 4, Appli
25	222	14.0	99	16 US-10-777-524-4	Sequence 4, Appli
26	222	14.0	99	17 US-10-777-521-4	Sequence 391, App
27	148.5	9.3	305	15 US-10-291-265-391	Sequence 104, App
28	146.5	9.2	305	10 US-09-786-753-104	Sequence 104, App
29	146.5	9.2	305	10 US-09-786-753-120	Sequence 120, App
30	146.5	9.2	305	15 US-10-291-265-863	Sequence 863, App
31	139	8.7	290	9 US-09-965-529-18	Sequence 18, Appli
32	139	8.7	290	10 US-09-969-680A-18	Sequence 18, Appli
33	139	8.7	290	14 US-10-227-884-40	Sequence 40, Appli
34	139	8.7	290	14 US-10-230-163-40	Sequence 40, Appli
35	139	8.7	290	14 US-10-230-338-40	Sequence 40, Appli
36	139	8.7	290	14 US-10-218-531-40	Sequence 40, Appli
37	139	8.7	290	14 US-10-230-414-40	Sequence 40, Appli
38	139	8.7	290	14 US-10-232-224-40	Sequence 40, Appli
39	139	8.7	290	14 US-10-216-159A-40	Sequence 40, Appli
40	139	8.7	290	14 US-10-218-849-40	Sequence 40, Appli
41	139	8.7	290	14 US-10-227-873-40	Sequence 40, Appli
42	139	8.7	290	14 US-10-227-883-40	Sequence 40, Appli
43	139	8.7	290	14 US-10-219-076-40	Sequence 40, Appli
44	139	8.7	290	14 US-10-230-434-40	Sequence 40, Appli
45	139	8.7	290	14 US-10-219-003-40	Sequence 40, Appli

ALIGNMENTS

RESULT 1
US-09-774-381-58
Sequence 58, Application US/09774381
Publication No. US20030082677A1
GENERAL INFORMATION:
APPLICANT: Holtzman, Douglas A.
APPLICANT: McCarthy, Sean J.
APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL EDIRF, MTR-1, LSP-1, TAP-1, AND PA-I MOLECULES
FILE REFERENCE: NMI-107CP2
CURRENT APPLICATION NUMBER: US/09/774,381
CURRENT FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 08/941,354
PRIOR FILING DATE: 1999-09-30
PRIOR APPLICATION NUMBER: 09/010,674
PRIOR FILING DATE: 1998-01-22
PRIOR APPLICATION NUMBER: 60/061,149
PRIOR FILING DATE: 1997-10-06
PRIOR APPLICATION NUMBER: 09/014,347
PRIOR FILING DATE: 1998-01-27
PRIOR APPLICATION NUMBER: 60/061,159
PRIOR FILING DATE: 1997-10-06
PRIOR APPLICATION NUMBER: 09/474,151
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 09/004,206
PRIOR FILING DATE: 1998-01-08
PRIOR APPLICATION NUMBER: 60/061,143
PRIOR FILING DATE: 1997-10-06
PRIOR APPLICATION NUMBER: 09/483,414
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: 09/213,571
PRIOR FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: 08/994,890
PRIOR FILING DATE: 1997-12-19

NUMBER OF SEQ ID NOS: 59
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 58
LENGTH: 303
TYPE: PRT
ORGANISM: Homo sapiens
US-09-774-381-58

Query Match 100.0%; Score 1591; DB 10; Length 303;
Best Local Similarity 100.0%; Pred. No. 5, 1e-126;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGRPLLPPLPLPPLPAPLPSPGSGSPSYLYGVTPQKHLASMGSGVEIPSPFYYPWE 60
DB 1 MGRPLLPPLPLPPLPAPLPSPGSGSPSYLYGVTPQKHLASMGSGVEIPSPFYYPWE 60
QY 61 LATAPDVRIISMRGRHFGHGFSTYSTRPPSIHKDYVNRFLFWTEGQKSGFLRISNLQKODQ 120
DB 61 LATAPDVRIISMRGRHFGHGFSTYSTRPPSIHKDYVNRFLFWTEGQKSGFLRISNLQKODQ 120
QY 121 SVYFCRVELDTRSSGRQOMOSIEGTSLSTQAVTTTTPRSSMTTWRLSSTTTTGLRV 180
DB 121 SVYFCRVELDTRSSGRQOMOSIEGTSLSTQAVTTTTPRSSMTTWRLSSTTTTGLRV 180
QY 181 TOGKRSDSMHISLETAIVGVAVAVTVLGIMILGICLLMRRRKGGQRTKATTPAREPFQ 240
DB 181 TOGKRSDSMHISLETAIVGVAVAVTVLGIMILGICLLMRRRKGGQRTKATTPAREPFQ 240
QY 241 NTEEPYENIRNEGQNTDPKLNPKDGIIVYASLASSTSPRAPPSHRPLKSPONETLYSV 300
DB 241 NTEEPYENIRNEGQNTDPKLNPKDGIIVYASLASSTSPRAPPSHRPLKSPONETLYSV 300
QY 301 LKA 303
DB 301 LKA 303

RESULT 2
US-10-290-631-2

Sequence 2, Application US/10290631
Publication No. US20030105303A1
GENERAL INFORMATION:

APPLICANT: Adema, Gosee Jan
Meyard, Linde
Gorman, Daniel M.
McClanahan, Terrill K.
Zurawski, Sandra M.
Zurawski, Gerard
Lanier, Lewis L.
Phillips Jr., Joseph H.

TITLE OF INVENTION: Isolated Mammalian Monocyte Cell Genes;
Related Reagents

NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:

ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA

ZIP: 94304-1104
COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/290, 631
FILING DATE: 08-No. US20030105303A1-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/985, 950
FILING DATE: 05-DEC-1997
APPLICATION NUMBER: US 60/041, 279

FILING DATE: 21-MARCH-1997
APPLICATION NUMBER: US 60/033, 181
FILING DATE: 16-DEC-1996
APPLICATION NUMBER: US 60/032, 252
FILING DATE: 06-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0670K
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 852-9196
TELEFAX: (650) 496-1204
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 303 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Query Match 100.0%; Score 1591; DB 14; Length 303;
Best Local Similarity 100.0%; Pred. No. 5, 1e-126;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGRPLLPPLPLPPLPAPLPSPGSGSPSYLYGVTPQKHLASMGSGVEIPSPFYYPWE 60
DB 1 MGRPLLPPLPLPPLPAPLPSPGSGSPSYLYGVTPQKHLASMGSGVEIPSPFYYPWE 60
QY 61 LATAPDVRIISMRGRHFGHGFSTYSTRPPSIHKDYVNRFLFWTEGQKSGFLRISNLQKODQ 120
DB 61 LATAPDVRIISMRGRHFGHGFSTYSTRPPSIHKDYVNRFLFWTEGQKSGFLRISNLQKODQ 120
QY 121 SVYFCRVELDTRSSGRQOMOSIEGTSLSTQAVTTTTPRSSMTTWRLSSTTTTGLRV 180
DB 121 SVYFCRVELDTRSSGRQOMOSIEGTSLSTQAVTTTTPRSSMTTWRLSSTTTTGLRV 180
QY 181 TOGKRSDSMHISLETAIVGVAVAVTVLGIMILGICLLMRRRKGGQRTKATTPAREPFQ 240
DB 181 TOGKRSDSMHISLETAIVGVAVAVTVLGIMILGICLLMRRRKGGQRTKATTPAREPFQ 240
QY 241 NTEEPYENIRNEGQNTDPKLNPKDGIIVYASLASSTSPRAPPSHRPLKSPONETLYSV 300
DB 241 NTEEPYENIRNEGQNTDPKLNPKDGIIVYASLASSTSPRAPPSHRPLKSPONETLYSV 300
QY 301 LKA 303
DB 301 LKA 303

RESULT 3
US-10-780-043-2

Sequence 2, Application US/10780043
Publication No. US20040137506A1
GENERAL INFORMATION:

APPLICANT: Bates, Elizabeth
APPLICANT: Fournier, Nathalie
APPLICANT: Chalus, Lionel
APPLICANT: Gattone, Pierre

TITLE OF INVENTION: MONOCYTE-DERIVED NUCLEIC ACIDS AND RELATED COMPOSITIONS AND METHOD

FILE REFERENCE: SF0977X

CURRENT APPLICATION NUMBER: US/10/780, 043

CURRENT FILING DATE: 2004-02-17

PRIOR APPLICATION NUMBER: US/09/869, 388

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 14

SOFTWARE: IBM PC compatible

SEQ ID NO 2

LENGTH: 303

TYPE: PRT

ORGANISM: homo sapiens
US-10-780-043-2


```

; SOFTWARE: IBM PC compatible
; SEQ ID NO 4
; LENGTH: 230
; TYPE: PR1
; ORGANISM: homo sapiens
US-10-780-043-4

Query Match      73.9%; Score 1176.5; DB 16; Length 230;
Best Local Similarity 75.9%; Pred. No. 3,76-91;
Matches 230; Conservative 0; Mismatches 0; Indels 73; Gaps 1,

Cy      1  MGRPLLPPLPLPLPPAFLPPSGSGSPSLVGTQPKHLSASGSGVEIPFSFYWME 60
        |||
Db      1  MGRPLLPPLPLPLPPAFLPPSGSGSPSLVGTQPKHLSASGSGVEIPFSFYWME 60

Cy      61  LATAPDVRI SMRGHFGQSFYSTRPESIHQDVNRLPLANTEGOKSGFLRISNLQKQDO 120
        |||
Db      61  LATAPDVRI SMRKRHFGQSFYSTRPESIHQDVNRLPLANTEGOKSGFLRISNLQKQDO 120

Cy      121  SVYFCRAVELDRSSGROQOSIECTKLSTIQAVTTTTQRPSSMTTWRLSSITTTTGLRV 180
        |||
Db      121  SVYFCRAVELDRSSGROQOSIECTKLSTIQ----- 151

Cy      181  TCGKRBD SMHISLETA VGAVAVTVLGIMILGLICLLRRRRKGGQRTKATTPARPEPQ 240
        |||
Db      152  -----GGQRTKATTPARPEPQ 167

```

Oy		241	NTEBPEYENIRNEGQNTDPLKNDKGDIYYASLALSSSTSPRAPPSRRLPKSPPONETLYSV	300
Dd		168	NTEBPEYENIRNEGQNTDKLNPKDDGIYYASLALSSSTSPRAPPSRRLPKSPONETLYSV	227
Oy		301	LKA 303	
Dd		228	LKA 230	

RESULT 7
US-10-309-290-110
Sequence 110, Application US/10309290
Publication No. US20040023241A1
GENERAL INFORMATION:
APPLICANT: Alsebrook II, John P.
APPLICANT: Anderson, David W.
APPLICANT: Boldog, Ferenc L.
APPLICANT: Burgess, Catherine E.
APPLICANT: Chillakuru, Rajeev A.
APPLICANT: Edinger, Shlomit R.
APPLICANT: Gerlach, Valerie L.
APPLICANT: Gorman, Linda
APPLICANT: Gould-Rothberg, Bonnie E.
APPLICANT: Guo, Xiaojia
APPLICANT: Jeffers, Michael E.
APPLICANT: Ji, Weizhen
APPLICANT: Li, Li
APPLICANT: Maiyanakar, Uriel M.
APPLICANT: Miller, Charles E.
APPLICANT: Murphrey, Ryan
APPLICANT: Patturajan, Meera
APPLICANT: Peyman, John A.
APPLICANT: Rastelli, Luca
APPLICANT: Rieger, Daniel K.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Smithson, Glenda
APPLICANT: Starling, Gary
APPLICANT: Taupier, Raymond J.
APPLICANT: Voss, Edward Z.
APPLICANT: Zhong, Haihong
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS FOR PREPARATION THEREOF
FILE REFERENCE: 21402-502A
CURRENT APPLICATION NUMBER: US/10/309,290
CURRENT FILING DATE: 2002-12-02
PRIORITY APPLICATION NUMBER: 60/336,600

Query Match	73.6%	Score 1171.5	DB 15	Length 230
Best Local Similarity	75.6%	Pred. No. 9.7e-91		
Matches 229; Conservative	0	Mismatches 1	Indels 73	Gaps 1

RESULT 8
US-10-309-290-112
Sequence 112, Application US/10309290
Publication No. US20040023241A1
GENERAL INFORMATION:
APPLICANT: Alabrook II, John P.
APPLICANT: Anderson, David W.
APPLICANT: Boldo, Ferenc L.
APPLICANT: Bungees, Catherine E.
APPLICANT: Chillaikutu, Rajeev A.
APPLICANT: Edinger, Shlomit R.
APPLICANT: Gerlach, Valerie L.
APPLICANT: Gorman, Linda
APPLICANT: Gould-Rothberg, Bonnie E.
APPLICANT: Guo, Xiaojie
APPLICANT: Jeffers, Michael E.

Query Match	63.5%	Score 1010.5;	DB 15;	Length 206;
Best Local Similarity	67.7%	Pred. No. 3.3e-77;		
Matches 205; Conservative	0;	Mismatches 1;	Indels 97;	Gaps 2

QY	1	MGRPLLPPLPLPLLPALFQPSGSGSGSGSYLYGTQPHLSASMGSGVEIPSPFYPMW	60
DB	1	MGRPLPLPLPLPLLPALFQPSGSGSGSGSYLYGTQPHLSASMGSGVEIPSPFYPMW	60
QY	61	LATAEDVRI SWRRGHFGSGSYSTRPPSIHKDYVNRFLNWTBQSGSGFLRISLNLOKODQ	120
DB	61	LAT-----SIHKDYVNRFLNWTBQSGSGFLRISLNLOKODQ	96
QY	121	SVYFRRVELDPRSSGRQOMOSIEGKLSITQAVTTTQAPSSMTTWRLSSTTTTGLRV	180
DB	97	SVYFRRVELDPRSSGRQOMOSIEGKLSITQ-----	127
QY	181	TQGRKRSWSHISLETAAGVAVAVTVLGMILGLICLRRRRKGGQRTKATTPAREPFO	240
DB	128	-----GQGRKATTPAREPFO	143
QY	241	NTEEPYENIRNEGQNTDPLNKDKDGIYVASLALSSSTS PRA PSHRPLKSPONETLYSV	300
DB	144	NTEEPYENIRNEGQNTDPLNKDKDGIYVASLALSSSTS PRA PSHRPLKSPONENILYSV	203

QY 301 LKA 303
Db 204 LKA 206

RESULT 9

US-09-774-381-44
; Sequence 44, Application US/09774381
; Publication No. US20030082677A1
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: McCarthy, Sean A.
; APPLICANT: Pan, Yang
; APPLICANT: Gearing, David P.
; TITLE OF INVENTION: NOVEL EDIPF, MTR-1, LSP-1, TAP-1, AND PA-I MOLECULES
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: WNT-107CP2
; CURRENT APPLICATION NUMBER: US/09/774,381
; CURRENT FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 08/941,354
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 09/010,674
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 60/061,149
; PRIOR FILING DATE: 1997-10-06
; PRIOR APPLICATION NUMBER: 09/014,347
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: 60/061,159
; PRIOR FILING DATE: 1997-10-06
; PRIOR APPLICATION NUMBER: 09/474,151
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 09/004,206
; PRIOR FILING DATE: 1998-01-08
; PRIOR APPLICATION NUMBER: 60/061,143
; PRIOR FILING DATE: 1997-10-06
; PRIOR APPLICATION NUMBER: 09/483,414
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 09/213,571
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 08/994,890
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-774-381-44

Query Match 61.2%; Score 973.5; DB 10; Length 226;
Best Local Similarity 82.5%; Pred. No. 5e-74;
Matches 188; Conservative 14; Mismatches 17; Indels 9; Gaps 2;
QY 1 MGRPLLLPPLPPLPAPFLOPSGSGPSYLYGVTPKHLASMGSGVEIPPSFYYPWE 60
Db 1 MGRPLLLPPLPPLPAPFLOPSGSGPSYLYGVTPKHLASMGSGVEIPPSFYYPWE 60
QY 61 LATAPDVRIISMRGHHGQSFYSTRPSIHKOYVNLFLNMTGQSGFLRISNLKQDQ 120
Db 61 LATAPDVRIISMRGHHGQSFYSTRPSIHKOYVNLFLNMTGQSGFLRISNLKQDQ 120
QY 121 SVYFCRVELDTRSSGROQMSIEGTKLSTQAVTTTQRPSSMTTWRLSSTTTGLRV 180
Db 121 SVYFCRVELDTRSSGROQMSIEGTKLSTQAVTTTQRPSSMTTWRLSSTTTGLRV 180
QY 181 TOGKRSDSMHISLETAAGVAVAVTVLGMILGICLLR-WRRRKGOQ 227
Db 173 TESGHSSEWHLSLDTAIVLAVAVLKVITLGLCLLMMWRRKGSR 220

RESULT 10
US-10-780-043-10
; Sequence 10, Application US/10780043

; Publication No. US20040137506A1
; GENERAL INFORMATION:
; APPLICANT: Bates, Elizabeth
; APPLICANT: Rounnier, Nathalie
; APPLICANT: Chalus, Lionel
; APPLICANT: Garione, Pierre
; TITLE OF INVENTION: MONOCYTE-DERIVED NUCLEIC ACIDS AND RELATED COMPOSITIONS AND METHOD
; FILE REFERENCE: SF0977X
; CURRENT APPLICATION NUMBER: US/10/780,043
; CURRENT FILING DATE: 2004-02-17
; PRIOR APPLICATION NUMBER: US/09/869,388
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: IBM PC compatible
; SEQ ID NO 10
; LENGTH: 226
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-780-043-10

Query Match 61.2%; Score 973.5; DB 16; Length 226;
Best Local Similarity 82.5%; Pred. No. 5e-74;
Matches 188; Conservative 14; Mismatches 17; Indels 9; Gaps 2;
QY 1 MGRPLLLPPLPPLPAPFLOPSGSGPSYLYGVTPKHLASMGSGVEIPPSFYYPWE 60
Db 1 MGRPLLLPPLPPLPAPFLOPSGSGPSYLYGVTPKHLASMGSGVEIPPSFYYPWE 60
QY 61 LATAPDVRIISMRGHHGQSFYSTRPSIHKOYVNLFLNMTGQSGFLRISNLKQDQ 120
Db 61 LATAPDVRIISMRGHHGQSFYSTRPSIHKOYVNLFLNMTGQSGFLRISNLKQDQ 120
QY 121 SVYFCRVELDTRSSGROQMSIEGTKLSTQAVTTTQRPSSMTTWRLSSTTTGLRV 180
Db 121 SVYFCRVELDTRSSGROQMSIEGTKLSTQAVTTTQRPSSMTTWRLSSTTTGLRV 180
QY 181 TOGKRSDSMHISLETAAGVAVAVTVLGMILGICLLR-WRRRKGOQ 227
Db 173 TESGHSSEWHLSLDTAIVLAVAVLKVITLGLCLLMMWRRKGSR 220

RESULT 11
US-09-745-763-106
; Sequence 106, Application US/09745763
; Patent No. US20020065394A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; McCoy, John M.
; Lavalie, Edward R.
; Collins-Racie, Lisa A.
; Evans, Cheryl
; Merberg, David
; Treacy, Maurice
; Spaulding, Vikki
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
; NUMBER OF SEQUENCES: 219
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/745,763
; FILING DATE: 18-Jun-2000
; CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:
 NAME: Sprunger, Suzanne A.
 REGISTRATION NUMBER: 41,323
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 498-8284
 TELEFAX: (617) 876-5851
 INFORMATION FOR SEQ ID NO: 106:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 226 amino acids
 TYPE: amino acid
 STRANDEDNESS: <unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 106:
 US-09-745-763-106

Query Match 60.8%; Score 967.5; DB 9; Length 226;
 Best Local Similarity 82.0%; Pred. No. 1,6e-73;
 Matches 187; Conservative 14; Mismatches 18; Indels 9; Gaps 2;

QY 1 MGRPLLLPLPLLPAPLQPSGSGPSYLYGVTOPKHLASMGSGVEIPFSFYPM 60
 DB 1 MGRPLLLPLLLLPAPLQPSGSGPSYLYGVTOPKHLASMGSGVEIPFSFYPM 60
 QY 61 LATAPDVASMRGPHGQSFYSTRPSIHQDVNRFLPNTTEGQSGFLISNLOKDO 120
 DB 61 LATAPDVASMRGPHGQSFYSTRPSIHQDVNRFLPNTTEGQSGFLISNLOKDO 120
 QY 121 SVYFCRVELDTRRSGRQOQSIKGTKLITTOAVTTTTPSSMTTWTWLSSTTTTGLRV 180
 DB 121 SVYFCRVELDTRRSGRQOQSIKGTKLITTOAVTTTTPSSMTTWTWLSSTTTTGLRV 172
 QY 181 TQGRKRSWSHISLETAVGVAVAATVGLMILGICLRL-WRRRKGOQ 227
 DB 173 TESKHSSEWSHISLDTAIRVALAVLKTIVILGILCLLMMWRRRKGRS 220

RESULT 12
 US-10-262-445-128
 ; Sequence 128, Application US/10262445
 ; Publication No. US20040014058A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alsebrook II, John
 ; APPLICANT: Burgess, Catherine
 ; APPLICANT: Caterton, Elina
 ; APPLICANT: Chant, John
 ; APPLICANT: Chaudhuri, Amitabha
 ; APPLICANT: Edinger, Shlomit
 ; APPLICANT: Gerlach, Valerie
 ; APPLICANT: Glot, Loic
 ; APPLICANT: Gorman, Linda
 ; APPLICANT: Guo, Xiaojia
 ; APPLICANT: Kekuda, Ramesh
 ; APPLICANT: Mezes, Peter
 ; APPLICANT: Milet, Isabelle
 ; APPLICANT: Ooi, Chean Eng
 ; APPLICANT: Paturejan, Meera
 ; APPLICANT: Rieger, Daniel
 ; APPLICANT: Spytek, Kimberly
 ; APPLICANT: Taupier Jr., Raymond J.
 ; APPLICANT: Zethusen, Bryan
 ; APPLICANT: Zhong, Hailong
 ; APPLICANT: Zhong, Wei
 ; TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS C
 ; FILE REFERENCE: 21402-462D
 ; CURRENT APPLICATION NUMBER: US/10/262,445
 ; CURRENT FILING DATE: 2002-10-01
 ; PRIOR APPLICATION NUMBER: 60/327,454
 ; PRIOR FILING DATE: 2001-10-05
 ; PRIOR APPLICATION NUMBER: 60/327,917
 ; PRIOR FILING DATE: 2001-10-09
 ; PRIOR APPLICATION NUMBER: 60/326,029

; PRIOR FILING DATE: 2001-10-09
 ; PRIOR APPLICATION NUMBER: 60/328,056
 ; PRIOR FILING DATE: 2001-10-09
 ; PRIOR APPLICATION NUMBER: 60/328,849
 ; PRIOR FILING DATE: 2001-10-12
 ; PRIOR APPLICATION NUMBER: 60/329,414
 ; PRIOR FILING DATE: 2001-10-15
 ; PRIOR APPLICATION NUMBER: 60/330,142
 ; PRIOR FILING DATE: 2001-10-17
 ; PRIOR APPLICATION NUMBER: 60/341,058
 ; PRIOR FILING DATE: 2001-10-22
 ; PRIOR APPLICATION NUMBER: 60/343,629
 ; PRIOR FILING DATE: 2001-10-24
 ; PRIOR APPLICATION NUMBER: 60/349,575
 ; PRIOR FILING DATE: 2001-10-29
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 133
 ; SOFTWARE: Curation version 0.1
 ; SEQ ID NO 128
 ; LENGTH: 227
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-262-445-128

Query Match 60.2%; Score 958; DB 15; Length 227;
 Best Local Similarity 80.8%; Pred. No. 1e-72;
 Matches 185; Conservative 15; Mismatches 19; Indels 10; Gaps 2;

QY 1 MGRPLLLPLPLLPAPLQPSGSGPSYLYGVTOPKHLASMGSGVEIPFSFYPM 60
 DB 1 MGRPLLLPLLLLPAPLQPSGSGPSYLYGVTOPKHLASMGSGVEIPFSFYPM 60
 QY 61 LATAPDVASMRGPHGQSFYSTRPSIHQDVNRFLPNTTEGQSGFLISNLOKDO 120
 DB 61 LATAPDVASMRGPHGQSFYSTRPSIHQDVNRFLPNTTEGQSGFLISNLOKDO 120
 QY 121 SVYFCRVELDTRRSGRQOQSIKGTKLITTOAVTTTTPSSMTTWTWLSSTTTTGLRV 180
 DB 121 SVYFCRVELDTRRSGRQOQSIKGTKLITTOAVTTTTPSSMTTWTWLSSTTTTGLRV 172
 QY 181 TQGRKRSWSHISLETAVGVAVAATVGLMILGICLRL-WRRRKGOQ 227
 DB 173 TESKHSSEWSHISLDTAIRVALAVLKTIVILGILCLLMMWRRRKGRS 221

RESULT 13
 US-10-780-043-6
 ; Sequence 6, Application US/10780043
 ; Publication No. US20040137506A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bates, Elizabeth
 ; APPLICANT: Fournier, Nathalie
 ; APPLICANT: Chaluis, Lionel
 ; APPLICANT: Garrone, Pierre
 ; TITLE OF INVENTION: MONOCYTE-DERIVED NUCLEIC ACIDS AND RELATED COMPOSITIONS AND METHO
 ; FILE REFERENCE: SP0977X
 ; CURRENT APPLICATION NUMBER: US/10/780,043
 ; CURRENT FILING DATE: 2004-02-17
 ; PRIOR APPLICATION NUMBER: US/09/869,388
 ; PRIOR FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: IBM PC compatible
 ; SEQ ID NO 6
 ; LENGTH: 227
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 ; US-10-780-043-6
 Query Match 60.2%; Score 958; DB 16; Length 227;
 Best Local Similarity 80.8%; Pred. No. 1e-72;
 Matches 185; Conservative 15; Mismatches 19; Indels 10; Gaps 2;
 QY 1 MGRPLLLPLPLLPAPLQPSGSGPSYLYGVTOPKHLASMGSGVEIPFSFYPM 60

